GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:51:02 ; Search time 14.5 Seconds
(without alignments)
798.519 Million cell updates/sec

Title: US-09-724-583-2
Perfect score: 818
Sequence: 1 MCSLPMARYYIIKYADQKAL.....QLTKESEPSARTKFYFEQSW 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	283	34.6	155	2	JC7104	interleukin-1 rece
2	260.5	31.8	178	2	C40956	interleukin-1 rece
3	257.5	31.5	178	2	A44610	interleukin-1 rece
4	241	29.5	177	2	A54377	interleukin-1 rece
5	238.5	29.2	177	2	A30368	interleukin-1 rece
6	238.5	29.2	180	2	A39386	interleukin-1 rece
7	137.5	16.8	267	2	S38373	interleukin-1 beta
8	134.5	16.4	267	1	JN0724	interleukin-1 beta
9	132	16.1	266	1	S23010	interleukin-1 beta
10	124.5	15.2	269	1	I55969	interleukin-1 beta
11	117	14.3	266	1	ICBO1B	interleukin-1 beta
12	110.5	13.5	268	1	A30584	interleukin-1 beta
13	104.5	12.8	269	1	ICHU1B	interleukin-1 beta
14	92	11.2	214	2	JC5646	interleukin-1 beta
15	89	10.9	3623	2	T09456	intrinsic factor-B
16	84.5	10.3	299	2	I49264	ubiquitinating enz
17	80	9.8	381	2	A75490	probable transamin
18	80	9.8	1092	2	S42798	fibronectin-bindin
19	76.5	9.4	520	1	A46661	leukotriene B4 ome
20	76	9.3	463	2	S44267	sulfate adenylyltr
21	76	9.3	1117	2	S33851	fibronectin-bindin
22	71.5	8.7	4302	2	A38971	polycystic kidney
23	71	8.7	599	2	I53395	antigen LEC-A - mo
24	71	8.7	7962	2	I38346	elastic titin - hu
25	70.5	8.6	827	1	FOMSIA	retrovirus-related
26	70	8.6	263	2	C83616	beta-ketoadipate e
27	70	8.6	331	2	E75067	aminopeptidase m42
28	70	8.6	348	2	C69399	N5,N10-methylenete
29	69.5	8.5	465	2	E71409	sulfate adenylyltr
30	69.5	8.5	532	2	B82354	deoxycytidylate de
31	69	8.4	339	2	S09264	Ig alpha chain C r
32	69	8.4	355	2	T47147	hypothetical prote
33	69	8.4	520	2	S45702	leukotriene-B4 20-
34	69	8.4	700	2	A84243	phosphoribosylform
35	68.5	8.4	256	2	T12999	aquaporin homolog
36	68.5	8.4	450	2	T45573	anthranilate N-hyd
37	68.5	8.4	557	4	EBRTMS	IgE-binding protei
38	68.5	8.4	656	2	E96713	hypothetical prote
39	68.5	8.4	729	2	JC5812	norbin - rat
40	68.5	8.4	892	1	S42228	replication licens
41	67.5	8.3	2403	2	T30875	PRP8 protein homol
42	67	8.2	398	2	F75417	L-sorbosone dehydr
43	67	8.2	622	2	T51223	hypothetical prote
44	67	8.2	665	2	H69101	archaeosine tRNA-r
45	67	8.2	832	2	S41889	beta-galactosidase

ALIGNMENTS

RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7104
R;Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A;Title: IL1HY1: A novel interleukin-1 receptor antagonist gene.
A;Reference number: JC7104; MUID:99443727
A;Accession: JC7104
A;Molecule type: mRNA
A;Residues: 1-155 <MUL>
A;Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C;Genetics:
A;Gene: il1hy1
A;Map position: 2q14
C;Keywords: macrophage

Query Match 34.6%; Score 283; DB 2; Length 155;
Best Local Similarity 45.7%; Pred. No. 8.3e-22;
Matches 63; Conservative 20; Mismatches 49; Indels 6; Gaps 3;

```
Qy      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
           | ||  : ||| |   |       |:|  :||| || :  |: ||:||||:||:|   :|
Db      17 KVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGGSQCLSCGVGQE- 75

Qy      77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
           |:| || ||| ||| | :|:  |||::   |     |:||:||||||   |  |||:||:
Db      76 PTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQ 135

Qy     137 ESE----PSARTKFYFEQ 150
             |      :  | |||:|
Db     136 LPENGGWNAPITDFYFQQ 153
```

RESULT 2
C40956
interleukin-1 receptor antagonist precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: C40956
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
A;Reference number: A40956; MUID:91271363
A;Accession: C40956
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <EIS>
A;Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929

```
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor

  Query Match             31.8%;  Score 260.5;  DB 2;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 2e-19;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: | .   |    |||  :|   :|   |  |||| ||  ||:||::
Db      45 NQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :  ||||:||| :| |  ||  |||| :| :|     |: | ||||||   |   || |
Db     100 DDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
       160 TNTPKEPCTVTKFYFQE 176


RESULT   3
A44610
interleukin-1 receptor antagonist precursor - mouse
N;Alternate names: IL-1Ra
C;Species: Mus musculus (house mouse)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: A44610; B40956; A49031; I56106; I52970
R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophag
A;Reference number: A44610; MUID:91316273
A;Accession: A44610
A;Molecule type: mRNA
A;Residues: 1-178 <MAT>
A;Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A;Reference number: A40956; MUID:91271363
A;Accession: B40956
A;Molecule type: DNA
A;Residues: 7-178 <EIS>
A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A;Title: Cloning, heterologous expression and characterization of murine interleukin 1 r
A;Reference number: A49031; MUID:92037824
A;Accession: A49031
A;Molecule type: mRNA
A;Residues: 23-178 <SHU>
A;Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
A;Experimental source: peritoneal macrophages, ICR strain
A;Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBIP:64085)
R;Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A;Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mappin
A;Reference number: I56106; MUID:91250712
A;Accession: I56106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-178 <RES>
A;Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A;Reference number: I52970; MUID:94271931
A;Accession: I52970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RE2>
A;Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
C;Genetics:
A;Gene: IL-1rn
A;Introns: 40/2; 70/1; 107/3
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

  Query Match             31.5%;  Score 257.5;  DB 2;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 4.1e-19;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    |||  :|   :|   |  |||| ||  ||:| ::
Db      45 NQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :  ||||:||| :| |  ||  |||| :|  |     |:|| ||||||   |  :|| |
Db     100 DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPEEPLIVTKFYFQE 176


RESULT   4
A54377
interleukin-1 receptor antagonist secreted form precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A54377; I46729
R;Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M
J. Biol. Chem. 269, 6962-6971, 1994
A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional ch
A;Reference number: A54377; MUID:94165101
A;Accession: A54377
A;Molecule type: mRNA
A;Residues: 1-177 <COM>
A;Cross-references: GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g545741
A;Experimental source: colon tissue
A;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
R;Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Ma
Immunology 77, 235-244, 1992
A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. P
A;Reference number: I46729; MUID:93052512
A;Accession: I46729
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-177 <GOT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             29.5%;  Score 241;  DB 2;  Length 177;
  Best Local Similarity   39.2%;  Pred. No. 2e-17;
  Matches   60;  Conservative   22;  Mismatches   57;  Indels   14;  Gaps    5;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVP--IF 58
           | :   | : :   :||  | |: ||: |     |    |:|  :|         |  :|
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPLE-------PQLLF 82

Qy      59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWP 118
           |||| |  ||:||:: :   | || ||| :| |  |:  |||| :|:||     |:|: |
Db      83 LGIQRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCP 142

Qy     119 GWFLCGPAEPQQPVQLTKESEPS-ARTKFYFEQ 150
           |||||   |  ||| ||   : |   |||||::
Db     143 GWFLCTALEADQPVSLTNTPDDSIVVTKFYFQE 175
```

```
RESULT   5
A30368
interleukin-1 receptor antagonist secreted form precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
C;Accession: A40956; I37894; A30368; S08160; S08159; A37822
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A;Reference number: A40956; MUID:91271363
A;Accession: A40956
A;Molecule type: DNA
A;Residues: 1-177 <EIS>
A;Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386
R;Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, R
Cytokine 4, 83-89, 1992
A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist g
A;Reference number: I37894; MUID:92338323
A;Accession: I37894
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <LEN>
A;Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J
J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tr
Nature 344, 633-638, 1990
A;Title: Purification, cloning, expression and biological characterization of an interle
A;Reference number: A30368; MUID:90220867
A;Accession: A30368
A;Molecule type: mRNA
A;Residues: 1-177 <CAR>
A;Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
Nature 343, 341-346, 1990
A;Title: Primary structure and functional expression from complementary DNA of a human i
A;Reference number: S08160; MUID:90136921
A;Accession: S08160
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-177 <EI2>
A;Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
R;Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; Ar
Nature 343, 336-340, 1990
A;Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
A;Reference number: S08159; MUID:90136920
A;Accession: S08159
A;Molecule type: protein
A;Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R;Bienkowski, M.J.; Eessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
J. Biol. Chem. 265, 14505-14511, 1990
A;Title: Purification and characterization of interleukin 1 receptor level antagonist pr
A;Reference number: A37822; MUID:90354444
A;Accession: A37822
A;Molecule type: protein
A;Residues: 26-52;70-77;122-127;170-175 <BIE>
A;Experimental source: culture medium, PMA-stimulated THP-1 cells
C;Comment: For an alternative splice form, see PIR:A39386
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
A;Introns: 39/2; 69/1; 106/3
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             29.2%;  Score 238.5;  DB 2;  Length 177;
  Best Local Similarity   40.9%;  Pred. No. 3.6e-17;
  Matches   56;  Conservative   18;  Mismatches   56;  Indels    7;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    |||  :|         :|||| ||  ||:||::
Db      44 NQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 98

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :  |||| ||| :| :  ::  || | :| ||     |:|| ||||||   |  ||| |
Db      99 DETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSL 158

Qy     135 TKESEPSAR-TKFYFEQ 150
           |   :    |||||::
Db     159 TNMPDEGVMVTKFYFQE 175


RESULT   6
A39386
interleukin-1 receptor antagonist, long intracellular splice form - human
N;Contains: interleukin-1 receptor antagonist, short intracellular splice form
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
C;Accession: I37893; A39386
R;Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Manto
J. Exp. Med. 182, 623-628, 1995
A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor
A;Reference number: I37893; MUID:95355865
A;Accession: I37893
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-180 <RES>
A;Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor an
A;Reference number: A39386; MUID:91219436
A;Accession: A39386
A;Molecule type: mRNA
A;Residues: 1-3,25-180 <HAS>
A;Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
C;Comment: For an alternative splice form, see PIR:A30368
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor
F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #s
F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice f

  Query Match             29.2%;  Score 238.5;  DB 2;  Length 180;
  Best Local Similarity   40.9%;  Pred. No. 3.7e-17;
  Matches   56;  Conservative   18;  Mismatches   56;  Indels    7;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    |||  :|         :|||| ||  ||:||::
Db      47 NQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 101

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :  |||| ||| :| :  ::  || | :| ||     |:|| ||||||   |  ||| |
Db     102 DETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSL 161

Qy     135 TKESEPSAR-TKFYFEQ 150
           |   :    |||||::
Db     162 TNMPDEGVMVTKFYFQE 178


RESULT   7
S38373
interleukin-1 beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S38373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O
```

```
Eur. J. Biochem. 217, 45-52, 1993
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and geneticall
A;Reference number: S38373; MUID:94039070
A;Accession: S38373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <VAN>
A;Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C;Genetics:
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C;Superfamily: interleukin-1


  Query Match             16.8%;  Score 137.5;  DB 2;  Length 267;
  Best Local Similarity   32.3%;  Pred. No. 1.4e-06;
  Matches   31;  Conservative   20;  Mismatches   44;  Indels    1;  Gaps    1;

Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: |||:| :  |:||  :: |:||||||:  : |   :   || |:::   :    |
Db     169 KIPVTLGIKGKNLYLSCVMKDDTPTLQLEDVD-PKSYPKRDMEKRFVFYKTEIKNRVEFE 227

Qy     114 AAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
           :| :| |::      |:|| |         | |  |
Db     228 SALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263


RESULT   8
JN0724
interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: JN0724
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be
A;Reference number: JN0724; MUID:93314975
A;Accession: JN0724
A;Molecule type: mRNA
A;Residues: 1-267 <HUE>
A;Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608
A;Experimental source: alveolar macrophage
C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processes i
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;115-267/Product: interleukin-1 beta #status predicted <IL1>
F;77/Binding site: myristate (Lys) (covalent) #status predicted


  Query Match             16.4%;  Score 134.5;  DB 1;  Length 267;
  Best Local Similarity   31.2%;  Pred. No. 2.8e-06;
  Matches   30;  Conservative   20;  Mismatches   45;  Indels    1;  Gaps    1;

Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: |||:| :  |:||  :  |:||||||:  : |   :   || |:::   :    |
Db     169 KIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYKTEIKNRVEFE 227

Qy     114 AAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
           :| :| |::      |:|| |         | |  |
Db     228 SALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263


RESULT   9
S23010
interleukin-1 beta precursor - sheep
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C;Accession: S23010; S43047; S13092; B61246
R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A;Reference number: S23010; MUID:92119335
A;Accession: S23010
A;Molecule type: mRNA
A;Residues: 1-266 <SEO>
A;Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an a
R;Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A;Reference number: S43047
A;Accession: S43047
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-63,'A',65-144,'L',146-266 <SAR>
A;Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274
R;Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A;Title: Nucleotide sequence of ovine interleukin-1 beta.
A;Reference number: S13092; MUID:91088326
A;Accession: S13092
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-61,'S',63,'A',65-144,'L',146-266 <FIS>
A;Cross-references: EMBL:X54796
A;Note: the authors translated the codon AGT for residue 62 as Arg
R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A;Reference number: A61246; MUID:92120716
A;Accession: B61246
A;Molecule type: mRNA
A;Residues: 1-144,'L',146-266 <AND>
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             16.1%;  Score 132;  DB 1;  Length 266;
  Best Local Similarity   25.4%;  Pred. No. 5.1e-06;
  Matches   34;  Conservative   28;  Mismatches   44;  Indels   28;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR---------------TKVPIFLG 60
           :||:|                | |: |  |   ||:: : |                |:|: ||
Db     127 EQKSL------------VLDSPCVLKALHLPSQEMSREVVFCMSFVQGEERDNKIPVALG 174

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           |:  :  |:||:  : |:||||:|:  ::|       || |:::   :    |:  :| |
Db     175 IRDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESVLYPNW 233

Qy     121 FLCGPAEPQQPVQL 134
           ::      ::|| |
Db     234 YISTSQIEEKPVFL 247


RESULT  10
I55969
interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: I55969; A24719; S13029
R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for
A;Reference number: I55969; MUID:87058957
A;Accession: I55969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RES>
```

```
A;Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398
R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A;Title: The murine interleukin 1-beta gene: structure and evolution.
A;Reference number: A24719; MUID:87117546
A;Accession: A24719
A;Molecule type: mRNA
A;Residues: 1-269 <TEL>
A;Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667
R;Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I.
FEBS Lett. 278, 98-102, 1991
A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by sel
A;Reference number: S13029; MUID:91130610
A;Accession: S13029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 118-269 <DAU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
C;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <IL1>


  Query Match             15.2%;  Score 124.5;  DB 1;  Length 269;
  Best Local Similarity   24.4%;  Pred. No. 3.1e-05;
  Matches   39;  Conservative   28;  Mismatches   52;  Indels   41;  Gaps    5;

Qy       1 MCSLPMAR-YYIIKYADQKALYTRD----------GQ----------LLVGDPVADNCC 38
           :| :|: : :| ::   ||:|   |          ||            : |:|  |
Db     115 VCDVPIRQLHYRLRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSND--- 171

Qy      39 AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATR 98
                       |:|: ||::| :  |:||  :  |:|||| |: :: |   :   |
Db     172 --------------KIPVALGLKGKNLYLSCVMKDGTPTLQLESVDPKQ-YPKKKMEKR 215

Qy      99 FTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKES 138
           | | :    |    |:| :| |::       :|| |   |
Db     216 FVFNKIEVKSKVEFESAEFPNWYISTSQAEHKPVFLGNNS 255


RESULT  11
ICBO1B
interleukin-1 beta precursor - bovine
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: JL0010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.;
Mol. Immunol. 25, 429-437, 1988
A;Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
A;Reference number: A94695; MUID:88318652
A;Accession: JL0010
A;Molecule type: mRNA
A;Residues: 1-266 <MAL>
A;Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A;Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A;Reference number: S01380; MUID:89016591
A;Accession: S01380
A;Molecule type: mRNA
A;Residues: 1-251,'A',253-266 <LEO>
A;Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C;Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             14.3%;  Score 117;  DB 1;  Length 266;
  Best Local Similarity   29.5%;  Pred. No. 0.00018;
  Matches   26;  Conservative   24;  Mismatches   36;  Indels    2;  Gaps    2;

Qy      48 RGLDR-TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSS 106
           :| :|  |:|: |||:  :  |:||:  : |:||||:|:  ::|       || |:::
Db     161 QGEERDNKIPVALGIKDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEI 219

Qy     107 GSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :    |:  :| |::      ::|| |
Db     220 KNTVEFESVLYPNWYISTSQIEERPVFL 247


RESULT  12
A30584
interleukin-1 beta precursor - rabbit
N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: A27714; A30584; JU0082; A32166
R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potenti
A;Reference number: A27714; MUID:88134238
A;Accession: A27714
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-268 <MOR>
R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello
J. Immunol. 142, 2299-2306, 1989
A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription dur
A;Reference number: A30584; MUID:89176242
A;Accession: A30584
A;Molecule type: mRNA
A;Residues: 1-268 <CAN>
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R;Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha a
A;Reference number: A94230; MUID:89315718
A;Accession: JU0082
A;Molecule type: mRNA
A;Residues: 1-268 <YOU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>


  Query Match             13.5%;  Score 110.5;  DB 1;  Length 268;
  Best Local Similarity   30.6%;  Pred. No. 0.00084;
  Matches   26;  Conservative   16;  Mismatches   42;  Indels    1;  Gaps    1;

Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: ||::| :  |:||  :: |:|||| |:    |   :   || | :         |
Db     170 KIPVALGLRGKNLYLSCVMKDDKPTLQLESVD-PNRYPKKKMEKRFVFNKIEIKDKLEFE 228

Qy     114 AAAWPGWFLCGPAEPQQPVQLTKES 138
           :| :| |::        || |   |
Db     229 SAQFPNWYISTSQTEYMPVFLGNNS 253


RESULT  13
ICHU1B
interleukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
```

C;Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev
A;Reference number: A25542; MUID:87040762
A;Accession: A25542
A;Molecule type: DNA; mRNA
A;Residues: 1-5,'K',7-269 <CLA>
A;Cross-references: GB:X04500; NID:g33788
A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
R;Bensi, G.; Raugei, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A;Title: Human interleukin-1 beta gene.
A;Reference number: A29019; MUID:87248099
A;Accession: A29019
A;Molecule type: DNA
A;Residues: 1-269 <BEN>
A;Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816
[redacted]uron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare
[redacted]c. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: A94023; MUID:85088517
A;Accession: A94023
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-269 <AUR>
A;Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.
Nature 315, 641-647, 1985
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A;Reference number: A93361; MUID:85240547
A;Accession: A93361
A;Molecule type: mRNA
A;Residues: 1-269 <MAR>
A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were confirm
R;Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: I51852
A;Accession: I51852
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hira
Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
[redacted]eference number: I52217; MUID:87156769
[redacted]Accession: I65200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <NIS>
A;Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov,
ii, S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin
A;Reference number: I38131; MUID:90249285
A;Accession: I38132
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <KOT>
A;Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R;Zsebo, K.M.; Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.
Blood 71, 962-968, 1988
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic
A;Reference number: A90732; MUID:88184226
A;Accession: B27616
A;Molecule type: protein
A;Residues: 117-123,'X',125-126,'X',128 <ZSE>
R;Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A;Title: The 31-kDa precursor of interleukin lalpha is myristoylated on specific lysines
A;Reference number: A48293; MUID:93348250
A;Contents: annotation; myristylation of lysines
R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
Biochim. Biophys. Acta 1118, 25-35, 1991
A;Title: The role of arginine residues in interleukin 1 receptor binding.
A;Reference number: S19608; MUID:92110334
A;Contents: annotation; type 1 IL-1 receptor interaction site
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R;Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A;Reference number: A50049; PDB:6I1B
A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R;Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution
A;Reference number: A44675; MUID:91159409
A;Contents: annotation; (1)H-NMR structural determination
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a
A;Reference number: A39774; MUID:91201363
A;Contents: annotation
R;Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A;Reference number: A50016; PDB:1I1B
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspa
J. Mol. Biol. 209, 779-791, 1989
A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom res
A;Reference number: A44666; MUID:90064532
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: GDB:IL1B
A;Cross-references: GDB:120094; OMIM:147720
A;Map position: 2q13-2q21
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop
F;117-269/Product: interleukin-1 beta #status experimental <IL1>
F;76/Binding site: myristate (Lys) (covalent) (partial) #status experimental
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 12.8%; Score 104.5; DB 1; Length 269;
Best Local Similarity 29.6%; Pred. No. 0.0035;
Matches 24; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

```
Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: ||::  :  |:||  :: |:|||| |: :  |   :   || | :    :   |
Db     171 KIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRFVFNKIEINNKLEFE 229

Qy     114 AAAWPGWFLCGPAEPQQPVQL 134
           :| :| |::        || |
Db     230 SAQFPNWYISTSQAENMPVFL 250
```

RESULT 14
JC5646
interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 20-Jun-2000
C;Accession: JC5646
R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa
Gene 177, 11-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-
A;Reference number: JC5646; MUID:97080493
A;Accession: JC5646
A;Molecule type: mRNA
A;Residues: 1-214 <KAT>
A;Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA22528.1; PID:g2463550

C;Comment: This protein mediates a variety of physiological response to infections and i
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce
C;Superfamily: interleukin-1

Query Match 11.2%; Score 92; DB 2; Length 214;
Best Local Similarity 28.4%; Pred. No. 0.052;
Matches 25; Conservative 18; Mismatches 43; Indels 2; Gaps 2;

Qy 48 RGLDRT-KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSS 106
Db 109 QGEEETDKIPVALGLKEKNLYLSCGMKDGKPTLQLETVD-PNTYPKRKMEKRFVFNKMEI 167

Qy 107 GSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
Db 168 KGNVEFESAMYPNWYISTSQAEKSPVFL 195

RESULT 15
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A;Reference number: Z16677; MUID:98241400
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
C;Genetics:
A;Map position: 10p12
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;436-467/Domain: EGF homology <EGF>

Query Match 10.9%; Score 89; DB 2; Length 3623;
Best Local Similarity 27.3%; Pred. No. 2.6;
Matches 33; Conservative 19; Mismatches 57; Indels 12; Gaps 5;

Qy 18 KALYTRDGQLLVGDPVADNCCAE-KIC--TLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
Db 2544 KVIFFTDGSRPYGGFTASYTSSEDAVCGGSLPNTPEGNFTSPGYDGVRNYSRNLNCEWTL 2603

Qy 75 EGPSLQLEDVNI--EELYKGGEEATRFTFFQSSSGSAFRLEAAAWP-GWFLCGPAEPQQP 131
Db 2604 SNPNQGNSSISIHFEDFYLESHQDCQFDVLE------FRVGDADGPLMWRLCGPSKPTLP 2657

Qy 132 V 132
Db 2658 L 2658

Search completed: May 10, 2002, 13:53:15
Job time: 133 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:50:47 ; Search time 12.64 Seconds
(without alignments)
270.609 Million cell updates/sec

Title: US-09-724-583-2
Perfect score: 818
Sequence: 1 MCSLPMARYYIIKYADQKAL.....QLTKESEPSARTKFYFEQSW 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	283	34.6	155	4	US-09-417-455-5	Sequence 5, Appli
2	260.5	31.8	178	3	US-09-000-630C-23	Sequence 23, Appl
3	260.5	31.8	178	3	US-08-862-730C-23	Sequence 23, Appl
4	260.5	31.8	178	4	US-09-417-455-10	Sequence 10, Appl
5	257.5	31.5	178	4	US-09-417-455-9	Sequence 9, Appli
6	255.5	31.2	178	3	US-09-000-630C-21	Sequence 21, Appl
7	255.5	31.2	178	3	US-08-862-730C-21	Sequence 21, Appl
8	248	30.3	151	3	US-09-000-630C-3	Sequence 3, Appli
9	248	30.3	151	3	US-08-862-730C-3	Sequence 3, Appli
10	248	30.3	154	3	US-09-000-630C-5	Sequence 5, Appli
11	248	30.3	154	3	US-08-862-730C-5	Sequence 5, Appli
12	248	30.3	176	3	US-09-000-630C-4	Sequence 4, Appli
13	248	30.3	176	3	US-08-862-730C-4	Sequence 4, Appli
14	241	29.5	177	3	US-09-000-630C-22	Sequence 22, Appl
15	241	29.5	177	3	US-08-862-730C-22	Sequence 22, Appl
16	241	29.5	177	4	US-09-417-455-11	Sequence 11, Appl
17	239.5	29.3	153	3	US-08-677-778B-1	Sequence 1, Appli
18	238.5	29.2	153	3	US-08-798-414-2	Sequence 2, Appli
19	238.5	29.2	153	4	US-09-131-247-2	Sequence 2, Appli
20	238.5	29.2	153	4	US-09-131-247-4	Sequence 4, Appli
21	238.5	29.2	156	1	US-08-476-860-10	Sequence 10, Appl
22	238.5	29.2	156	2	US-08-910-733-10	Sequence 10, Appl
23	238.5	29.2	156	2	US-08-910-884-10	Sequence 10, Appl
24	238.5	29.2	159	1	US-08-459-811-2	Sequence 2, Appli
25	238.5	29.2	159	2	US-08-484-598-2	Sequence 2, Appli
26	238.5	29.2	159	2	US-08-459-092-2	Sequence 2, Appli
27	238.5	29.2	159	2	US-08-459-814-2	Sequence 2, Appli
28	238.5	29.2	159	2	US-08-425-232-2	Sequence 2, Appli
29	238.5	29.2	159	2	US-08-471-227-3	Sequence 3, Appli
30	238.5	29.2	159	2	US-08-479-140-2	Sequence 2, Appli
31	238.5	29.2	159	3	US-08-477-143-2	Sequence 2, Appli
32	238.5	29.2	159	4	US-09-417-455-14	Sequence 14, Appl
33	238.5	29.2	177	1	US-08-422-655-2	Sequence 2, Appli
34	238.5	29.2	177	2	US-08-809-185-2	Sequence 2, Appli
35	238.5	29.2	177	3	US-09-000-630C-20	Sequence 20, Appl
36	238.5	29.2	177	3	US-08-862-730C-20	Sequence 20, Appl
37	238.5	29.2	177	3	US-09-128-155-14	Sequence 14, Appl
38	238.5	29.2	177	4	US-09-417-455-30	Sequence 30, Appl
39	238.5	29.2	180	1	US-08-476-860-13	Sequence 13, Appl
40	238.5	29.2	180	2	US-08-910-733-13	Sequence 13, Appl
41	238.5	29.2	180	2	US-08-910-884-13	Sequence 13, Appl
42	238.5	29.2	388	4	US-09-131-247-16	Sequence 16, Appl
43	238.5	29.2	389	4	US-09-131-247-14	Sequence 14, Appl
44	177.5	21.7	169	2	US-08-790-032-2	Sequence 2, Appli
45	177.5	21.7	169	3	US-09-069-619-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-417-455-5
; Sequence 5, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-5

Query Match 34.6%; Score 283; DB 4; Length 155;
Best Local Similarity 45.7%; Pred. No. 1.8e-26;
Matches 63; Conservative 20; Mismatches 49; Indels 6; Gaps 3;

```
Qy      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
           | ||  : ||| |   |       |:|  :||| || :  |: ||:||||:||:|   :|
Db      17 KVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGGSQCLSCGVGQE- 75

Qy      77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
           |:| || ||| ||| | :|:  |||::   |     |:||:||||||   |  |||:||:
```

```
Db      76 PTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQ 135

Qy     137 ESE----PSARTKFYFEQ 150
           |     :  | |||:|
Db     136 LPENGGWNAPITDFYFQQ 153


RESULT   2
US-09-000-630C-23
; Sequence 23, Application US/09000630C
; Patent No. 6018029
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  178 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rat IL-1ra sequence
US-09-000-630C-23


  Query Match             31.8%;  Score 260.5;  DB 3;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 1.1e-23;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    |||  :|   :|   |  |||| ||  ||:||::
Db      45 NQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   ||||:||| :| |  ||  |||| :| :|     |: | ||||||   |   || |
Db     100 DDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPKEPCTVTKFYFQE 176


RESULT   3
US-08-862-730C-23
; Sequence 23, Application US/08862730C
; Patent No. 6063600
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  178 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rat IL-1ra sequence
US-08-862-730C-23


  Query Match             31.8%;  Score 260.5;  DB 3;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 1.1e-23;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    |||  :|   :|   |  |||| ||  ||:||::
Db      45 NQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   ||||:||| :| |  ||  |||| :| :|     |: | ||||||   |   || |
Db     100 DDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPKEPCTVTKFYFQE 176


RESULT   4
US-09-417-455-10
; Sequence 10, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Pace, Ann
;  TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
;  FILE REFERENCE: 28110/36328
;  CURRENT APPLICATION NUMBER: US/09/417,455
;  CURRENT FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER: US 09/348,942
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: PCT/US99/04291
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: US 09/287,210
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: US 09/251,370
;  PRIOR FILING DATE: 1999-02-17
;  PRIOR APPLICATION NUMBER: US 09/229,591
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 09/127,698
;  PRIOR FILING DATE: 1998-07-31
;  PRIOR APPLICATION NUMBER: US 09/099,818
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: US 09/082,364
;  PRIOR FILING DATE: 1998-05-20
;  PRIOR APPLICATION NUMBER: US 09/079,909
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 09/055,010
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 30
```

```
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 178
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-417-455-10


  Query Match             31.8%;  Score 260.5;  DB 4;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 1.1e-23;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    ||| :|   :|   |  |||| ||  ||:||::
Db      45 NQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   ||||:||| :| |  ||  |||| :| :|     |: | ||||||   |   || |
Db     100 DDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPKEPCTVTKFYFQE 176


RESULT   5
US-09-417-455-9
; Sequence 9, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Pace, Ann
;  TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
;  FILE REFERENCE: 28110/36328
;  CURRENT APPLICATION NUMBER: US/09/417,455
;  CURRENT FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER: US 09/348,942
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: PCT/US99/04291
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: US 09/287,210
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: US 09/251,370
;  PRIOR FILING DATE: 1999-02-17
;  PRIOR APPLICATION NUMBER: US 09/229,591
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 09/127,698
;  PRIOR FILING DATE: 1998-07-31
;  PRIOR APPLICATION NUMBER: US 09/099,818
   PRIOR FILING DATE: 1998-06-19
   PRIOR APPLICATION NUMBER: US 09/082,364
   PRIOR FILING DATE: 1998-05-20
;  PRIOR APPLICATION NUMBER: US 09/079,909
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 09/055,010
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 178
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-417-455-9


  Query Match             31.5%;  Score 257.5;  DB 4;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 2.5e-23;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    ||| :|   :|   |  |||| ||  ||:| ::
Db      45 NQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   ||||:||| :| |  ||  |||| :| :|     |:|| ||||||   |  :|| |
Db     100 DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPEEPLIVTKFYFQE 176


RESULT   6
US-09-000-630C-21
; Sequence 21, Application US/09000630C
; Patent No. 6018029
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  178 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  mouse IL-1ra sequence
US-09-000-630C-21


  Query Match             31.2%;  Score 255.5;  DB 3;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 4.4e-23;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNCCAE-KICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |   | ||  :|   :|   |  |||| ||  ||:| ::
Db      45 NQKTFYLRNNQLIAGYLQGPNIKLEGKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   ||||:||| :| |  ||  |||| :| :|     |:|| ||||||   |  :|| |
Db     100 DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPEEPLIVTKFYFQE 176


RESULT   7
US-08-862-730C-21
; Sequence 21, Application US/08862730C
; Patent No. 6063600
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
```

```
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  178 amino acids
;      TYPE:  amino acid
,      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  mouse IL-1ra sequence
US-08-862-730C-21


  Query Match             31.2%;  Score 255.5;  DB 3;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 4.4e-23;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy      16 DQKALYTRDGQLLVGDPVADNCCAE-KICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |      |   | ||  :|   :|   |  |||| ||  ||:| ::
Db      45 NQKTFYLRNNQLIAGYLQGPNIKLEGKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 99

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   ||||:||| :| |  ||  |||| :|  |     |:|| ||||||   |  :|| |
Db     100 DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 159

Qy     135 TK-ESEPSARTKFYFEQ 150
           |    ||   |||||::
Db     160 TNTPEEPLIVTKFYFQE 176


RESULT   8
US-09-000-630C-3
; Sequence 3, Application US/09000630C
; Patent No. 6018029
; GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  151 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  mature peptide
US-09-000-630C-3


  Query Match             30.3%;  Score 248;  DB 3;  Length 151;
  Best Local Similarity   39.7%;  Pred. No. 2.8e-22;
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           |  :   | : :   :||  | |: ||: |      |    ||:  :|         :|||
Db       8 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 59

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |||| ||| :| |  ::  |||| | ||     |:|| |||
Db      60 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 119

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  :|| ||   | :   |||||::
Db     120 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 150


RESULT   9
US-08-862-730C-3
; Sequence 3, Application US/08862730C
; Patent No. 6063600
; GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  151 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  mature peptide
US-08-862-730C-3


  Query Match             30.3%;  Score 248;  DB 3;  Length 151;
  Best Local Similarity   39.7%;  Pred. No. 2.8e-22;
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           |  :   | : :   :||  | |: ||: |      |    ||:  :|         :|||
Db       8 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 59

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |||| ||| :| |  ::  |||| | ||     |:|| |||
Db      60 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 119

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  :|| ||   | :   |||||::
Db     120 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 150
```

```
RESULT  10
US-09-000-630C-5
; Sequence 5, Application US/09000630C
; Patent No. 6018029
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  154 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cleaved IL-1ra peptide from fusion construct
US-09-000-630C-5


  Query Match             30.3%;  Score 248;  DB 3;  Length 154;
  Best Local Similarity   39.7%;  Pred. No. 2.9e-22;
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           |  :    |  :  :    :||  | |: ||: |      |     ||:  :|          :|||
Db      11 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 62

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |||| ||| :| |  ::  ||||  | ||     |:|| |||
Db      63 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 122

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  :|| ||   | :   |||||::
Db     123 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 153


RESULT  11
US-08-862-730C-5
; Sequence 5, Application US/08862730C
; Patent No. 6063600
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  154 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cleaved IL-1ra peptide from fusion construct
US-08-862-730C-5


  Query Match             30.3%;  Score 248;  DB 3;  Length 154;
  Best Local Similarity   39.7%;  Pred. No. 2.9e-22;
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           |  :    |  :  :    :||  | |: ||: |      |     ||:  :|          :|||
Db      11 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 62

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |||| ||| :| |  ::  ||||  | ||     |:|| |||
Db      63 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 122

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  :|| ||   | :   |||||::
Db     123 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 153


RESULT  12
US-09-000-630C-4
; Sequence 4, Application US/09000630C
; Patent No. 6018029
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  176 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  IL-1ra full length peptide
US-09-000-630C-4


  Query Match             30.3%;  Score 248;  DB 3;  Length 176;
  Best Local Similarity   39.7%;  Pred. No. 3.5e-22;
```

```
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           | :   | : :   :||  | |: ||: |     |    ||:  :|          :|||
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 84

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |||| ||| :| |  ::  ||||  | ||     |:|| |||
Db      85 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 144

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  :|| ||   | :   |||||::
Db     145 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 175


RESULT  13
US-08-862-730C-4
; Sequence 4, Application US/08862730C
; Patent No. 6063600
; GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  176 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  IL-1ra full length peptide
; US-08-862-730C-4


  Query Match           30.3%;  Score 248;  DB 3;  Length 176;
  Best Local Similarity   39.7%;  Pred. No. 3.5e-22;
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           | :   | : :   :||  | |: ||: |     |    ||:  :|          :|||
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 84

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |||| ||| :| |  ::  ||||  | ||     |:|| |||
Db      85 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 144

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  :|| ||   | :   |||||::
Db     145 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 175


RESULT  14
US-09-000-630C-22
; Sequence 22, Application US/09000630C
; Patent No. 6018029
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  177 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rabbit IL-1ra sequence
US-09-000-630C-22


  Query Match           29.5%;  Score 241;  DB 3;  Length 177;
  Best Local Similarity   39.2%;  Pred. No. 2.5e-21;
  Matches   60;  Conservative   22;  Mismatches   57;  Indels   14;  Gaps    5;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVP--IF 58
           | :   | : :   :||  | |: ||: |     |    |:|  :|         |  :|
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPLE-------PQLLF 82

Qy      59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWP 118
           |||| |  ||:||:: :   | || ||| :| |  |:  |||| :|:||     |:|: |
Db      83 LGIQRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCP 142

Qy     119 GWFLCGPAEPQQPVQLTKESEPS-ARTKFYFEQ 150
           |||||   |  ||| ||   : |   ||||::
Db     143 GWFLCTALEADQPVSLTNTPDDSIVVTKFYFQE 175


RESULT  15
US-08-862-730C-22
; Sequence 22, Application US/08862730C
; Patent No. 6063600
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
```

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rabbit IL-1ra sequence
US-08-862-730C-22

Query Match 29.5%; Score 241; DB 3; Length 177;
Best Local Similarity 39.2%; Pred. No. 2.5e-21;
Matches 60; Conservative 22; Mismatches 57; Indels 14; Gaps 5;

```
Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVP--IF 58
           |  :   | : :   :||  | |: ||: |     |   |:|  :|        |  :|
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPLE-------PQLLF 82

Qy      59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWP 118
           |||| |  ||:||:: :   | || ||| :| |  |:  |||| :|:||     |:|: |
Db      83 LGIQRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCP 142

       119 GWFLCGPAEPQQPVQLTKESEPS-ARTKFYFEQ 150
           |||||   |  ||| ||   : |   |||||::
Db     143 GWFLCTALEADQPVSLTNTPDDSIVVTKFYFQE 175
```

Search completed: May 10, 2002, 13:52:52
Job time: 125 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:50:17 ; Search time 23.86 Seconds
(without alignments)
471.883 Million cell updates/sec

Title: US-09-724-583-2
Perfect score: 818
Sequence: 1 MCSLPMARYYIIKYADQKAL.....QLTKESEPSARTKFYFEQSW 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	818	100.0	152	22	AAE05840	Human FIL-1 theta
2	818	100.0	152	22	AAB19922	Human interleukin-
3	818	100.0	169	22	AAB19923	Human interleukin-
4	818	100.0	200	22	AAB19924	Human interleukin-
5	729.5	89.2	154	22	AAB84999	Human interleukin-
6	657	80.3	152	22	AAE05841	Mouse FIL-1 theta
7	657	80.3	152	22	AAB19925	Mouse interleukin-
8	587	71.8	112	22	AAE05839	Human FIL-1 theta
9	309	37.8	156	19	AAW86284	Rodent interleukin
10	309	37.8	156	20	AAY28407	Mouse interleukin
11	309	37.8	156	21	AAY92260	Murine IL-1 homolo
12	309	37.8	156	21	AAY45061	Murine TANGO-93 pr
13	307	37.5	154	22	AAE06663	Mouse interleukin-
14	307	37.5	155	21	AAY96937	Murine IL-1 recept
15	307	37.5	155	22	AAB35261	Murine IL-1L1. Mu
16	307	37.5	155	22	AAB66672	Invention related
17	307	37.5	155	22	AAB48828	Murine interleukin
18	289	35.3	155	21	AAY92256	Human IL-1 homolog
19	283	34.6	154	22	AAB35263	Interleukin-IL1 re
20	283	34.6	155	20	AAY28408	Human interleukin
21	283	34.6	155	21	AAY96936	Human IL-1 recepto
22	283	34.6	155	21	AAY92257	Human IL-1 homolog
23	283	34.6	155	21	AAY45062	Human TANGO-93 pro
24	283	34.6	155	22	AAE06655	Human interleukin-
25	283	34.6	155	22	AAB87601	Human PRO4342. Ho
26	283	34.6	155	22	AAB35260	Human IL-1L1. Hom
27	283	34.6	155	22	AAB35262	Interleukin-IL1 re
28	283	34.6	155	22	AAB66664	Protein encoded by
29	283	34.6	157	22	AAB35264	Interleukin-IL1 re
30	282	34.5	155	21	AAY92255	Generic human IL-1
31	280	34.2	155	20	AAY43526	A human interleuki
32	276	33.7	155	21	AAY92253	Generic human IL-1
33	276	33.7	155	21	AAY92254	Hhuman IL-1 homolo
34	260.5	31.8	178	20	AAY43528	Rat interleukin-1
35	260.5	31.8	178	20	AAY33280	Rat interleukin-1
36	260.5	31.8	178	22	AAB66666	Rat interleukin-1
37	260	31.8	178	20	AAY43527	Mouse interleukin-
38	257.5	31.5	178	20	AAY33281	Mouse interleukin-
39	257.5	31.5	178	22	AAB66665	Mouse interleukin-
40	248	30.3	151	20	AAW81060	Amino acid sequenc
41	248	30.3	154	20	AAW81062	fusion protein of
42	248	30.3	176	20	AAW81061	Amino acid sequenc
43	241	29.5	177	20	AAY43529	Rabbit interleukin
44	241	29.5	177	22	AAB66667	Rabbit interleukin
45	240.5	29.4	159	16	AAR73642	iCIL-1ra. Homo sa

ALIGNMENTS

RESULT 1
AAE05840
ID AAE05840 standard; Protein; 152 AA.
XX
AC AAE05840;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human FIL-1 theta full-length protein.
XX
KW Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;
KW insulin dependent diabetes mellitus; lymphoma; microbial infection;
KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;
KW tibial muscular dystrophy; inflammation; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO200155211-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02514.
XX
PR 27-JAN-2000; 2000US-0178389.
PR 11-APR-2000; 2000US-0195962.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE;
XX
DR WPI; 2001-457718/49.
DR N-PSDB; AAD11148.
XX
PT isolated FIL-1 theta polypeptide to induce or inhibit the induction of

```
PT   fever and to stimulate the immune system for the treatment of microbial
PT   infections -
XX
PS   Claim 14; Page 5; 65pp; English.
XX
CC   The invention relates to interleukin-1 (IL-1) family ligand designated
CC   as FIL-1 theta polypeptides and nucleic acid molecules encoding such
CC   polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin
CC   dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/
CC   lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1
CC   theta polypeptides are used to activate and/or inhibit the activation
CC   of vascular endothelial cells and lymphocytes; the induction of local
CC   tissue destruction and fever; the stimulation of macrophages and
CC   vascular endothelial cells to produce IL-6 and the induction of
CC   prostaglandins. They are also used to treat inflammation and microbial
CC   infections. FIL-1 theta DNA is useful in antisense therapy and gene
CC   therapy. The present sequence is human FIL-1 theta full-length protein.

     Sequence   152 AA;


  Query Match             100.0%;  Score 818;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-86;
  Matches  152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mcslpmaryyiikyadqkalytrdgqllvgdpvadnccaekictlpnrgldrtkvpiflg 60

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 iqggsrclacveteegpslqledvnieelykggeeatrftffqssssgsafrleaaawpgw 120

Qy     121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||||||
Db     121 flcgpaepqqpvqltkesepsartkfyfeqsw 152


RESULT   2
AAB19922
ID   AAB19922 standard; Protein; 152 AA.
XX
AC   AAB19922;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 (short version).

KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 44
FT                   /note= "polymorphism in nucleotide sequence, alters
FT                           Thr-44 to Ile"
FT   Misc-difference 51
FT                   /note= "polymorphism in nucleotide sequence, alters
FT                           Asp-51 to Ala"
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   N-PSDB; AAA89175, AAA89176.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Example 5; Page 130-132; 158pp; English.
XX
CC   The present sequence is that of human interleukin-1 Hy2 (IL-1 Hy2),
CC   a novel member of the interleukin-1 receptor antagonist family.
CC   The sequence is predicted from isolated cDNA clones (see AAA89175 and
CC   AAA89176).  Potential polymorphisms in the coding region may alter
CC   the sequence, specifically changing Thr-44 to Ile and Asp-51 to
CC   Ala, which may affect the biological activity of the molecule.
CC   An alternative, extended open reading frame encodes a 200-amino
CC   acid protein (see AAB19924). IL-1 Hy2 polypeptides and polynucleotides
CC   are used to treat cancers involving elevated levels of IL-1, such as
CC   breast adenocarcinoma, brain tumours, melanoma, giant cell tumours
CC   of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or
CC   squamous cell carcinoma, and inflammatory disease mediated by
CC   interleukin-18 (all claimed).  They can also be used to diagnose,
CC   prevent or treat shock, thrombosis, acute pancreatitis, arthritis,
CC   vasculitis, lupus, immune complex glomerulonephritis, pancreatic
CC   cell damage, allograft and xenograft transplantation, graft versus
CC   host disease, inflammatory bowel disease, bone degenerative
CC   diseases, diabetes and neurodegenerative disorders.
XX
SQ   Sequence   152 AA;


  Query Match             100.0%;  Score 818;  DB 22;  Length 152;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-86;
  Matches  152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mcslpmaryyiikyadqkalytrdgqllvgdpvadnccaekictlpnrgldrtkvpiflg 60

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 iqggsrclacveteegpslqledvnieelykggeeatrftffqssssgsafrleaaawpgw 120

Qy     121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||||||
Db     121 flcgpaepqqpvqltkesepsartkfyfeqsw 152


RESULT   3
AAB19923
ID   AAB19923 standard; Protein; 169 AA.
XX
AC   AAB19923;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 (extended form, partial sequence).
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
```

```
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   N-PSDB; AAA89175.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Example 5; Page 134-145; 158pp; English.
XX
CC   The present sequence is that of a human interleukin-1 Hy2 (IL-1 Hy2)
CC   non-full length polypeptide, as predicted from an isolated cDNA
CC   clone (see AAA89175).  A 200-amino acid full-length sequence is given
CC   in AAB19924.  IL-1 Hy2 is a novel member of the interleukin-1 receptor
CC   antagonist family.  IL-1 Hy2 polypeptides and polynucleotides are
CC   used to treat cancers involving elevated levels of IL-1, such as
CC   breast adenocarcinoma, brain tumours, melanoma, giant cell tumours
CC   of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or
CC   squamous cell carcinoma, and inflammatory disease mediated by
CC   interleukin-18 (all claimed).  They can also be used to diagnose,
CC   prevent or treat shock, thrombosis, acute pancreatitis, arthritis,
CC   vasculitis, lupus, immune complex glomerulonephritis, pancreatic
CC   cell damage, allograft and xenograft transplantation, graft versus
CC   host disease, inflammatory bowel disease, bone degenerative
CC   diseases, diabetes and neurodegenerative disorders.
XX
SQ   Sequence   169 AA;
```

```
  Query Match             100.0%;  Score 818;  DB 22;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-86;
  Matches  152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 mcslpmaryyiikyadqkalytrdgqllvgdpvadnccaekictlpnrgldrtkvpiflg 77

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 iqggsrclacveteegpslqledvnieelykggeeatrftffqssssgsafrleaaawpgw 137

      121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||||||
Db     138 flcgpaepqqpvqltkesepsartkfyfeqsw 169
```

```
RESULT   4
AAB19924
ID   AAB19924 standard; Protein; 200 AA.
XX
AC   AAB19924;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 (long version).
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   N-PSDB; AAA89177, AAA89178.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Example 5; Page 144-145; 158pp; English.
XX
CC   The present sequence is that of human interleukin-1 Hy2 (IL-1 Hy2),
CC   a novel member of the interleukin-1 receptor antagonist family.
CC   The sequence is predicted from the genomic DNA sequence (see
CC   AAA89177) and a predicted cDNA sequence (see AAA89178).  An alternative
CC   open reading frame (see AAA89176) encodes a 152 polypeptide (see
CC   AAB19922).  IL-1 Hy2 polypeptides and polynucleotides are used to
CC   treat cancers involving elevated levels of IL-1, such as
CC   breast adenocarcinoma, brain tumours, melanoma, giant cell tumours
CC   of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or
CC   squamous cell carcinoma, and inflammatory disease mediated by
CC   interleukin-18 (all claimed).  They can also be used to diagnose,
CC   prevent or treat shock, thrombosis, acute pancreatitis, arthritis,
CC   vasculitis, lupus, immune complex glomerulonephritis, pancreatic
CC   cell damage, allograft and xenograft transplantation, graft versus
CC   host disease, inflammatory bowel disease, bone degenerative
CC   diseases, diabetes and neurodegenerative disorders.
XX
SQ   Sequence   200 AA;
```

```
  Query Match             100.0%;  Score 818;  DB 22;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-86;
  Matches  152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49 mcslpmaryyiikyadqkalytrdgqllvgdpvadnccaekictlpnrgldrtkvpiflg 108

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 iqggsrclacveteegpslqledvnieelykggeeatrftffqssssgsafrleaaawpgw 168

Qy     121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||||||
Db     169 flcgpaepqqpvqltkesepsartkfyfeqsw 200
```

```
RESULT   5
AAB84999
ID   AAB84999 standard; Protein; 154 AA.
XX
AC   AAB84999;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human interleukin-1 receptor antagonist (NOVINTRA A) polypeptide.
XX
KW   NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW   gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW   cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW   antibacterial; cerebroprotective; antidiabetic; antiarthritic;
```

KW antiasthmatic; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200140291-A2.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US33029.
XX
PR 06-DEC-1999; 99US-0169056.
PR 09-DEC-1999; 99US-0169866.
PR 09-DEC-1999; 99US-0169886.
PR 10-DEC-1999; 99US-0170252.
PR 12-JAN-2000; 2000US-0175740.
PR 05-DEC-2000; 2000US-0170252.
XX
(CURA-) CURAGEN CORP.

Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;
PI Mezes PS;
XX
DR WPI; 2001-374790/39.
DR N-PSDB; AAF83868.
XX
PT Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders -
XX
PS Claim 1; Fig 9B; 138pp; English.
XX
CC The invention provides novel polypeptides (NOVX) selected from human
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC antagonist proteins (NOVINTRA A and B). The invention also provides
CC methods in which a NOVX polypeptide, polynucleotide and antibody are
CC used in the detection, prevention and treatment of a broad range of
CC pathological states. NOVTRAN can be used to treat is a cell signaling
CC disorder such as cancer, immune response disorder, hematopoietic
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC central nervous system, breast, colon, ovary, kidney, prostate and
CC thyroid. NOVGON can be used to treat reproductive development disorder,
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC to treat bone metabolism or structure disorder, inflammatory response
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC arthritis and cancer. The present sequence represents the NOVINTRA A
CC polypeptide.
XX
SQ Sequence 154 AA;

Query Match 89.2%; Score 729.5; DB 22; Length 154;
Best Local Similarity 93.9%; Pred. No. 3.8e-76;
Matches 139; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

```
Qy     12 IKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACV 71
           |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db      7 ikyadqkalytrdgqllvgdpvadnccaekicilpnrglartkvpiflgiqggsrclacv 66

Qy     72 ETEEGPSLQLE-------DVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCG 124
           ||||||||||        ||||||||||||||||||||||||||||||||||||||||
Db     67 eteegpslqlepstlppqdvnieelykggeeatrftffqsssgsafrleaaawpgwflcg 126

Qy    125 PAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||
Db    127 paepqqpvqltkesepsartkfyfeqsw 154
```

RESULT 6
AAE05841
ID AAE05841 standard; Protein; 152 AA.
XX
AC AAE05841;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mouse FIL-1 theta protein.
XX
KW Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;
KW insulin dependent diabetes mellitus; lymphoma; microbial infection;
KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;
KW tibial muscular dystrophy; inflammation; gene therapy; mouse.
XX
OS Mus musculus.
XX
PN WO200155211-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02514.
XX
PR 27-JAN-2000; 2000US-0178389.
PR 11-APR-2000; 2000US-0195962.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE;
XX
DR WPI; 2001-457718/49.
DR N-PSDB; AAD11158.
XX
PT isolated FIL-1 theta polypeptide to induce or inhibit the induction of
PT fever and to stimulate the immune system for the treatment of microbial
PT infections -
XX
PS Claim 17; Page 6; 65pp; English.
XX
CC The invention relates to interleukin-1 (IL-1) family ligand designated
CC as FIL-1 theta polypeptides and nucleic acid molecules encoding such
CC polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin
CC dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/
CC lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1
CC theta polypeptides are used to activate and/or inhibit the activation
CC of vascular endothelial cells and lymphocytes; the induction of local
CC tissue destruction and fever; the stimulation of macrophages and
CC vascular endothelial cells to produce IL-6 and the induction of
CC prostaglandins. They are also used to treat inflammation and microbial
CC infections. FIL-1 theta DNA is useful in antisense therapy and gene
CC therapy. The present sequence is mouse FIL-1 theta protein.
XX
SQ Sequence 152 AA;

Query Match 80.3%; Score 657; DB 22; Length 152;
Best Local Similarity 82.1%; Pred. No. 8.5e-68;
Matches 124; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

```
Qy      1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
          |||||||||||||| | |||||||:||||:||| :||   ||:| ||||||||:|||||||
Db      1 mcslpmaryyiikdahqkalytrngqlllgdpdsdnyspekvcilpnrgldrskvpiflg 60

Qy     61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
          :|||| |||||:| ||| |||||||||:||||||: ||||||| | |||||||||| |||
Db     61 mqggscclacvktregpllqledvniedlykggeqttrftffqrslgsafrleaaacpgw 120

Qy    121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQS 151
          |||||||||||||||||||  |:|||| |
Db    121 flcgpaepqqpvqltkesepsthtefyfems 151
```

RESULT 7
AAB19925
ID AAB19925 standard; Protein; 152 AA.
XX

```
AC   AAB19925;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Mouse interleukin-1 Hy2.
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy.
XX
OS   Mus sp.
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   N-PSDB; AAA89179, AAA89180.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Example 9; Page 152-153; 158pp; English.
XX
CC   The present sequence is that of mouse interleukin-1 Hy2 (IL-1 Hy2),
CC   as predicted from the genomic DNA sequence (see AAA89179).  IL-1 Hy2
CC   is a novel member of the interleukin-1 receptor antagonist family.
CC   The predicted mouse and human (see AAB19922) IL-1 Hy2 polypeptides
CC   share 81.7% homology.  Murine genomic DNA can be used to generate
CC   transgenic animals which overexpress IL-1 Hy2 protein or have the
CC   IL-2 Hy2 gene knocked out.  Human IL-1 Hy2 polypeptides and
CC   polynucleotides are used to treat cancers involving elevated levels
CC   of IL-1, such as breast adenocarcinoma, brain tumours, melanoma,
CC   giant cell tumours of bone, acute myelogenous leukaemia, oral
CC   epidermoid carcinoma or squamous cell carcinoma, and inflammatory
CC   disease mediated by interleukin-18 (claimed).
XX
     Sequence   152 AA;
```

```
  Query Match             80.3%;  Score 657;  DB 22;  Length 152;
  Best Local Similarity   82.1%;  Pred. No. 8.5e-68;
  Matches  124;  Conservative   10;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
           |||||||||||||| | |||||||:||||:||| :||   ||:| ||||||||:|||||||
Db       1 mcslpmaryyiikdahqkalytrngqlllgdpdsdnyspekvcilpnrgldrskvpiflg 60

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           :|||| |||||:| ||| |||||||||:|||||: |||||| | |||||||||| |||
Db      61 mqggscclacvktregpllqledvniedlykggeqttrftffqrslgsafrleaaacpgw 120

Qy     121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQS 151
           |||||||||||||||||||  |:|||| |
Db     121 flcgpaepqqpvqltkesepsthtefyfems 151
```

```
RESULT   8
AAE05839
ID   AAE05839 standard; Protein; 112 AA.
XX
```

```
AC   AAE05839;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Human FIL-1 theta protein.
XX
KW   Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;
KW   insulin dependent diabetes mellitus; lymphoma; microbial infection;
KW   ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;
KW   tibial muscular dystrophy; inflammation; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO200155211-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02514.
XX
PR   27-JAN-2000; 2000US-0178389.
PR   11-APR-2000; 2000US-0195962.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE;
XX
DR   WPI; 2001-457718/49.
DR   N-PSDB; AAD11147.
XX
PT   isolated FIL-1 theta polypeptide to induce or inhibit the induction of
PT   fever and to stimulate the immune system for the treatment of microbial
PT   infections -
XX
PS   Claim 1; Page 4; 65pp; English.
XX
CC   The invention relates to interleukin-1 (IL-1) family ligand designated
CC   as FIL-1 theta polypeptides and nucleic acid molecules encoding such
CC   polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin
CC   dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/
CC   lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1
CC   theta polypeptides are used to activate and/or inhibit the activation
CC   of vascular endothelial cells and lymphocytes; the induction of local
CC   tissue destruction and fever; the stimulation of macrophages and
CC   vascular endothelial cells to produce IL-6 and the induction of
CC   prostaglandins. They are also used to treat inflammation and microbial
CC   infections. FIL-1 theta DNA is useful in antisense therapy and gene
CC   therapy. The present sequence is human FIL-1 theta protein.
XX
SQ   Sequence   112 AA;
```

```
  Query Match             71.8%;  Score 587;  DB 22;  Length 112;
  Best Local Similarity   98.2%;  Pred. No. 6.7e-60;
  Matches  110;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      41 KICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFT 100
           ||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 kicilpnrglartkvpiflgiqggsrclacveteegpslqledvnieelykggeeatrft 60

Qy     101 FFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ffqsssgsafrleaaawpgwflcgpaepqqpvqltkesepsartkfyfeqsw 112
```

```
RESULT   9
AAW86284
ID   AAW86284 standard; Protein; 156 AA.
XX
AC   AAW86284;
XX
DT   19-FEB-1999  (first entry)
XX
DE   Rodent interleukin (IL)-1 delta polypeptide.
```

```
XX
KW   Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW   inflammatory response; immune system; diagnosis; agonist; antagonist;
KW   chemokine.
XX
OS   Mus sp.
XX
PN   WO9847921-A1.
XX
PD   29-OCT-1998.
XX
PF   17-APR-1998;   98WO-US06879.
XX
PR   06-AUG-1997;   97US-0055111.
PR   21-APR-1997;   97US-0837627.
XX
PA   (SCHE ) SCHERING CORP.

     Bazan JF,  Hedrick JA,  Kastelein RA,  Sana TR;

DR   WPI; 1998-609976/51.
DR   N-PSDB; AAV71958.
XX
PT   Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT   regulating the immune system and inflammatory responses
XX
PS   Claim 1; Pages 89-90; 113pp; English.
XX
CC   This represents a rodent interleukin (IL)-1 delta polypeptide. The
CC   invention relates to a recombinant polypeptide that specifically binds
CC   polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC   segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC   IL polypeptides are used to regulate a cell involved in an inflammatory
CC   response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC   used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC   the corresponding nucleic acids regulate development and/or the immune
CC   system, and can be used to diagnose and treat conditions associated with
CC   abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC   epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC   IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC   epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC   protein with another cytokine or chemokine.
XX
SQ   Sequence   156 AA;


  Query Match             37.8%;  Score 309;  DB 19;  Length 156;
  Best Local Similarity   45.2%;  Pred. No. 1.1e-27;
  Matches   70;  Conservative   23;  Mismatches   56;  Indels    6;  Gaps    3;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
           |  |  |  : :| :  | ||  : ||| |   |:     |:|  :||| || :  |: |
Db       1 mmvlsgalcfrmkdsalkvlylhnnqllagglhaekvikgeeisvvpnraldaslspvil 60

Qy      60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
           |:||||:||:|  ||:|| |:|| ||| ||| | :|:  |||::   |     |:|||:||
Db      61 gvqggsqclsc-gtekgpilklepvnimelylgakesksftfyrrdmgltssfesaaypg 119

Qy     120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
           ||||   |  |||:||:  |  |     | |||:|
Db     120 wflctspeadqpvrltqipedpawdapitdfyfqq 154


RESULT  10
AAY28407
ID   AAY28407 standard; Protein; 156 AA.
XX
AC   AAY28407;
XX
DT   28-SEP-1999  (first entry)
XX
DE   Mouse interleukin 1 delta.
XX
KW   Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;
KW   insulin-dependent diabetes mellitus; wrinkly skin syndrome;
KW   T-cell leukemia; lymphoma; tibial muscular dystrophy.
XX
OS   Mus musculus.
XX
PN   WO9935268-A1.
XX
PD   15-JUL-1999.
XX
PF   08-JAN-1999;   99WO-US00514.
XX
PR   01-JUN-1998;   98US-0087393.
PR   09-JAN-1998;   98US-0071074.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE;
XX
DR   WPI; 1999-458310/38.
DR   N-PSDB; AAX89431.
XX
PT   Murine and Human interleukin 1 delta DNA, polypeptides and its
PT   fragments, useful as molecular weight markers
XX
PS   Claim 1; Page 67; 72pp; English.
XX
CC   The present sequence represents mouse interleukin 1 delta (IL-1 delta).
CC   IL-1 delta proteins are useful for the determination of the molecular
CC   weight of a sample protein. The protein and its fragments are useful as
CC   controls for peptide fragmentation. This is useful for determining the
CC   isoelectric point of a sample protein. Antibodies generated against
CC   IL-1 delta and its fragmented peptides can be used to enhance the
CC   accuracy of these molecular weight markers to determine the apparent
CC   molecular eight and isoelectric point of a sample protein. IL-1 delta
CC   can be used to screen for potential inhibitors of activity associated
CC   with IL-1 delta counter-structure molecules. IL-1 delta can also be used
CC   as therapeutic agents for the treatment of diseases mediated by IL-1
CC   delta. IL-1 delta may be used as a reagent in studying the interleukin 1
CC   (IL-1) signalling pathway, or as a reagent to block IL-1 signalling. The
CC   IL-1 delta coding sequences can be used to identify human chromosome 2,
CC   and to identify genes associated with certain diseases, especially with
CC   region 2q11-12, including glaucoma, ectodermal dysplasia, insulin-
CC   dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukemia/
CC   lymphoma and tibial muscular dystrophy.
XX
SQ   Sequence   156 AA;


  Query Match             37.8%;  Score 309;  DB 20;  Length 156;
  Best Local Similarity   45.2%;  Pred. No. 1.1e-27;
  Matches   70;  Conservative   23;  Mismatches   56;  Indels    6;  Gaps    3;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
           |  |  |  : :| :  | ||  : ||| |   |:     |:|  :||| || :  |: |
Db       1 mmvlsgalcfrmkdsalkvlylhnnqllagglhaekvikgeeisvvpnraldaslspvil 60

Qy      60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
           |:||||:||:|  ||:|| |:|| ||| ||| | :|:  |||::   |     |:|||:||
Db      61 gvqggsqclsc-gtekgpilklepvnimelylgakesksftfyrrdmgltssfesaaypg 119

Qy     120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
           ||||   |  |||:||:  |  |     | |||:|
Db     120 wflctspeadqpvrltqipedpawdapitdfyfqq 154


RESULT  11
AAY92260
ID   AAY92260 standard; Protein; 156 AA.
XX
AC   AAY92260;
XX
DT   10-AUG-2000  (first entry)
```

```
XX
DE   Murine IL-1 homologue, zilla3.
XX
KW   Generic; interleukin-1; IL-1; homologue; zilla3; anti-inflammatory;
KW   antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;
KW   antirheumatic; osteopathic; antipsoriatic; antibacterial; cytostatic;
KW   immunosuppressive; antiulcer; antidiabetic; nephrotropic; vasotropic;
KW   vulnerary; 2q14.
XX
OS   Mus musculus.
XX
PN   WO200020595-A1.
XX
PD   13-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23533.
XX
PR   08-OCT-1998;   98US-0169745.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
     Sheppard PO, West RR, Clegg CH;

     WPI; 2000-303780/26.
DR   N-PSDB; AAA09198.
XX
PT   Proteins useful for treatment of inflammatory conditions such as
PT   rheumatoid arthritis and psoriasis are agonists or antagonists forms of
PT   new interleukin-1 homologue
XX
PS   Example 7; Page 59-60; 64pp; English.
XX
CC   This shows an interleukin-1 (IL-1) homologue, designated zilla3. A 350
CC   bp probe generated from the DNA sequence by PCR using AAA09199-200 was
CC   used to analyze human northern blots.
CC   It is believed that zilla3 acts through IL-1 receptors. In general,
CC   zilla3 proteins having a Lys residue at position 148 will have
CC   anti-inflammatory activity (e.g. AAY92256), whilst those having Asp
CC   (see AAY92254) or Glu at this position will have pro-inflammatory
CC   action. Zilla3 is used to modulate an immune response in an animal
CC   (claimed). Antagonists zilla3 forms may be used to treat or prevent
CC   chronic inflammatory diseases such as rheumatoid arthritis,
CC   osteoarthritis and Lyme arthritis, psoriasis, to reduce tissue damage
CC   after ischemia, to treat septic shock, graft-versus-host disease and
CC   leukemia. The antagonists may also alleviate inflammatory bowel disease
CC   including Crohn's disease and ulcerative colitis, insulin-dependent
CC   diabetes mellitus, acute pancreatitis, glomerulonephritis and cerebral
CC   ischemia. Agonist forms of zilla3 may promote wound healing by IL-1
CC   effects on growth factor secretion and cell proliferation. They may also
     treat infections, especially gastrointestinal infections.

     Sequence   156 AA;


  Query Match             37.8%;  Score 309;  DB 21;  Length 156;
  Best Local Similarity   45.2%;  Pred. No. 1.1e-27;
  Matches   70;  Conservative   23;  Mismatches   56;  Indels    6;  Gaps    3;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
           |  |  |  : :| :  | ||  : ||| |   |:     |:|  :||| || :  |: |
Db       1 mmvlsgalcfrmkdsalkvlylhnnqllagglhaekvikgeeisvvpnraldaslspvil 60

Qy      60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
           |:||||:||:|  ||:|| |:|| ||| ||| | :|:  |||::   |     |:||:||
Db      61 gvqggsqclsc-gtekgpilklepvnimelylgakesksftfyrrdmgltssfesaaypg 119

Qy     120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
           ||||   |  |||:||:  |  |     | |||:|
Db     120 wflctspeadqpvrltqipedpawdapitdfyfqq 154


RESULT  12
AAY45061
ID   AAY45061 standard; Protein; 156 AA.
XX
AC   AAY45061;
XX
DT   31-MAY-2000  (first entry)
XX
DE   Murine TANGO-93 protein.
XX
KW   TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer;
KW   Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
KW   immunosuppressive; antirheumatic; antiarthritic; antipsoriatic; asthma;
KW   antiinflammatory; antibacterial; antiulcer; cytostatic; immunomodulator;
KW   osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
KW   graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;
KW   septic shock; cachexia; Crohn's disease; chronic myelogenous leukaemia;
KW   liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
KW   autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
KW   systemic lupus erythematosus; forensic; transgenic animal.
XX
OS   Mus sp.
XX
PN   WO200008045-A2.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US17886.
XX
PR   07-AUG-1998;   98US-0131263.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Pan Y;
XX
DR   WPI; 2000-205669/18.
DR   N-PSDB; AAZ50811.
XX
PT   Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful
PT   for treating a variety of cellular processes e.g. asthma, rheumatoid
PT   arthritis, psoriasis and autoimmune diseases
XX
PS   Claim 9; Fig 1; 113pp; English.
XX
CC   The present sequence is the murine TANGO-93, a secreted protein, that
CC   belongs to the cytokine superfamily. It plays a role similar to secreted
CC   Interleukin-1 receptor antagonist (IL-1ra) and its expression is
CC   developmentally regulated in liver, heart and bone marrow. TANGO-93
CC   modulates immune mediated inflammation and IL-1 gene or protein
CC   expression. TANGO-93 is useful as a modulating agent for regulating
CC   cellular processes like asthma, graft vs-host disease, rheumatoid
CC   arthritis, psoriasis, inflammatory bowel disease, septic shock,
CC   ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,
CC   cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,
CC   cachexia, and autoimmune diseases e.g. myasthenia gravis, autoimmune
CC   diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences
CC   are useful in forensic biology, for diagnostic and prognostic assays,
CC   prophylactic and therapeutic treatment and pharmacogenomics. The DNA
CC   sequences are useful as hybridisation probes and primers, for isolation
CC   of TANGO-93 sequence and for the creation of transgenic animals.
XX
SQ   Sequence   156 AA;


  Query Match             37.8%;  Score 309;  DB 21;  Length 156;
  Best Local Similarity   45.2%;  Pred. No. 1.1e-27;
  Matches   70;  Conservative   23;  Mismatches   56;  Indels    6;  Gaps    3;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
           |  |  |  : :| :  | ||  : ||| |   |:     |:|  :||| || :  |: |
Db       1 mmvlsgalcfrmkdsalkvlylhnnqllagglhaekvikgeeisvvpnraldaslspvil 60

Qy      60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
           |:||||:||:|  ||:|| |:|| ||| ||| | :|:  |||::   |     |:||:||
Db      61 gvqggsqclsc-gtekgpilklepvnimelylgakesksftfyrrdmgltssfesaaypg 119
```

```
Qy     120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
           ||||   |  |||:||:  |  |     | |||:|
Db     120 wflctspeadqpvrltqipedpawdapitdfyfqq 154


RESULT  13
AAE06663
ID   AAE06663 standard; Protein; 154 AA.
XX
AC   AAE06663;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Mouse interleukin-1delta (IL-1delta) protein.
XX
KW   Mouse; interleukin-1delta; IL-1delta; virucide; hepatotropic; fever;
     immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
     autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
     psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS   Mus sp.
XX
PN   WO200157219-A2.
XX
PD   09-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US03285.
XX
PR   02-FEB-2000; 2000US-0179638.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Debets JEMA,  Timans JC,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 2001-488886/53.
XX
PT   Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT   polypeptide useful for treating conditions exhibiting abnormal
PT   expression of interleukin such as immunological disorders, tumor and
PT   allergy -
XX
PS   Disclosure; Fig 1; 103pp; English.
XX
CC   The invention relates to recombinant antigenic interleukin-1 like
CC   molecules and their corresponding nucleic acid sequences, designated
CC   as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC   IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC   abnormal expression of the interleukin such as immunological disorders,
CC   tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC   allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC   tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC   HIV). The invention also relates to methods of using the composition
CC   containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC   utilities. IL-1delta is used as an immunogen for the production of
CC   antisera or antibodies specific, e.g., capable of distinguishing between
CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present sequence is mouse
CC   interleukin-1delta (IL-1delta) protein related to the invention.
XX
SQ   Sequence   154 AA;

  Query Match             37.5%;  Score 307;  DB 22;  Length 154;
  Best Local Similarity   47.8%;  Pred. No. 1.9e-27;
  Matches   66;  Conservative   20;  Mismatches   46;  Indels    6;  Gaps    3;

Qy      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
           | ||  : ||| |   |:     |:|  :||| || :  |: ||:||||:||:|  ||:|
           *

Db      16 kvlylhnnqllagglhaekvikgeeisvvpnraldaslspvilgvqggsqclsc-gtekg 74

Qy      77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
           | |:|| ||| ||| | :|:  |||::   |     |:||:||||||   | |||:||:
Db      75 pilklepvnimelylgakesksftfyrrdmgltssfesaaypgwflctspeadqpvrltq 134

Qy     137 ESEPSA----RTKFYFEQ 150
             |  |     | |||:|
Db     135 ipedpawdapitdfyfqq 152


RESULT  14
AAY96937
ID   AAY96937 standard; Protein; 155 AA.
XX
AC   AAY96937;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Murine IL-1 receptor antagonist 3.
XX
KW   mIL-1Ra3; interleukin-1 receptor antagonist-3; IL-1lp; osteopathic;
KW   interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW   anti-arthritic; antimicrobial; respiratory; anti-ischemic; vaccine;
KW   dermatalogical; immunomodulatory; gastrointestinal; gene therapy.
XX
OS   Mus sp.
XX
PN   WO200039297-A2.
XX
PD   06-JUL-2000.
XX
PF   22-DEC-1999;   99WO-US30720.
XX
PR   23-DEC-1998;   98US-0113430.
PR   22-JAN-1999;   99US-0116843.
PR   13-APR-1999;   99US-0129122.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Goddard A,  Pan J;
XX
DR   WPI; 2000-452395/39.
DR   N-PSDB; AAA51599.
XX
PT   Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT   preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS   Claim 22; Fig 9A-B; 143pp; English.
XX
CC   An isolated nucleic acid molecule encoding an interleukin-1-like
CC   polypeptide (IL-1lp) that retains one or more activities of the peptide
CC   from which it is derived, such as the IL-18R binding activity of a human
CC   interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC   nucleic acids may be used in molecular engineering applications, e.g.
CC   hybridization assays and chromosome and gene mapping studies, for
CC   recombinantly producing the IL-1lp polypeptide or for producing gene
CC   knock out animals to study the role of the protein in metabolism and
CC   disease processes (conversely, gene therapy protocols may be used to
CC   supplement a patients production of the polypeptide or to rectify
CC   mutations that lead to the production of in active peptides). The
CC   peptides produced may be used to screen for and produce modulators (e.g.
CC   antibodies) of IL-1lp protein expression and activity which may be use
CC   to treat disorders associated with inappropriate IL-1lp expression and
CC   activity, such as inflammatory disorders, asthma, arthritis,
CC   osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC   syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC   psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ   Sequence   155 AA;

  Query Match             37.5%;  Score 307;  DB 21;  Length 155;
```

Best Local Similarity 47.8%; Pred. No. 1.9e-27;
Matches 66; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

```
Qy      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
           | ||  : ||| |   |:     |:|  :||| || :  |: ||:||||:||:|  ||:|
Db      17 kvlylhnnqllagglhaekvikgeeisvvpnraldaslspvilgvqggsqclsc-gtekg 75

Qy      77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
           | |:|| ||| ||| | :|:  |||::   |     |:||:||||||   |  |||:||:
Db      76 pilklepvnimelylgakesksftfyrrdmgltssfesaaypgwflctspeadqpvrltq 135

Qy     137 ESEPSA----RTKFYFEQ 150
             |  |     | |||:|
Db     136 ipedpawdapitdfyfqq 153
```

RESULT 15
AAB35261
ID AAB35261 standard; Protein; 155 AA.
XX
AC AAB35261;

08-MAY-2001 (first entry)

DE Murine IL-IL1.
XX
KW Mouse; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
KW osteoporosis; systemic lupus erythematosus.
XX
OS Mus sp.
XX
PN WO200105974-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-US19508.
XX
PR 16-JUL-1999; 99US-0144298.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Nicklin M, Barton J;
XX
DR WPI; 2001-091974/10.
XX
PT Nucleic acids encoding human and murine interleukin-1L1 polypeptides
PT useful for controlling inflammatory processes -

Claim 11; Fig 3; 150pp; English.

CC The present invention provides the protein and coding sequences of the
CC human and murine interleukin-IL1 (IL-IL1) proteins. The IL-IL1 gene is
CC located between the IL-1beta and IL-1receptor genes at human chromosome
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
CC of heart disease, cancer and inflammatory diseases such as rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
CC severe periodontal disease and pregnancy complications. The present
CC sequence is the murine IL-IL1 protein.
XX
SQ Sequence 155 AA;

Query Match 37.5%; Score 307; DB 22; Length 155;
Best Local Similarity 47.8%; Pred. No. 1.9e-27;
Matches 66; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

```
Qy      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
           | ||  : ||| |   |:     |:|  :||| || :  |: ||:||||:||:|  ||:|
Db      17 kvlylhnnqllagglhaekvikgeeisvvpnraldaslspvilgvqggsqclsc-gtekg 75

Qy      77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
           | |:|| ||| ||| | :|:  |||::   |     |:||:||||||   |  |||:||:
Db      76 pilklepvnimelylgakesksftfyrrdmgltssfesaaypgwflctspeadqpvrltq 135

Qy     137 ESEPSA----RTKFYFEQ 150
             |  |     | |||:|
Db     136 ipedpawdapitdfyfqq 153
```

Search completed: May 10, 2002, 13:52:33
Job time: 136 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 19, 2002, 04:46:47 ; Search time 2153.14 Seconds
(without alignments)
6393.869 Million cell updates/sec

Title: US-09-724-583-1
Perfect score: 1020
Sequence: 1 cagggatcagggttccagga.....acctctaaaaaaaaaaaaaa 1020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	714.8	70.1	900	11	AY026753	AY026753 Homo sapi
c	2	250.2	24.5	285	10	BI051175	BI051175 CM2-GN028
c	3	244.2	23.9	589	12	AQ766579	AQ766579 HS_2192_B
	4	168.6	16.5	574	9	BE067002	BE067002 PM0-BT034
c	5	137.2	13.5	507	9	AI889529	AI889529 wn05g02.x
c	6	128	12.5	459	9	AI393136	AI393136 tg41c11.x
c	7	127.4	12.5	392	9	AA417044	AA417044 zu13d02.s
c	8	126.2	12.4	718	12	AQ780593	AQ780593 HS_3138_A
c	9	125	12.3	612	12	AQ356956	AQ356956 CITBI-E1-
	10	122.2	12.0	533	12	AQ442721	AQ442721 HS_5116_B
	11	121	11.9	526	12	AQ318555	AQ318555 RPCI11-90
c	12	116.6	11.4	375	9	AA447609	AA447609 zw82d06.s
c	13	115.8	11.4	670	12	AG087298	AG087298 Pan trogl
c	14	115.4	11.3	634	12	B54722	B54722 CIT-HSP-384
c	15	114.6	11.2	525	12	AQ405885	AQ405885 HS_5043_B
	16	111.6	10.9	439	12	AQ112190	AQ112190 CIT-HSP-2
	17	111.6	10.9	1051	11	AK009741	AK009741 Mus muscu
	18	111.6	10.9	1199	11	AK008977	AK008977 Mus muscu
	19	110.8	10.9	726	10	BI089828	BI089828 602855071
	20	110.8	10.9	858	10	BI090567	BI090567 602855674
	21	110.8	10.9	932	9	AL545100	AL545100 AL545100
	22	109.8	10.8	539	12	AQ418783	AQ418783 RPCI-11-2
	23	109.2	10.7	603	10	BF793888	BF793888 602255284
c	24	108.2	10.6	668	12	AQ626032	AQ626032 CITBI-E1-
c	25	107.2	10.5	430	9	AA194145	AA194145 zr37g04.s
c	26	106.6	10.5	702	12	AQ627034	AQ627034 CITBI-E1-
c	27	106.6	10.5	705	12	AQ624891	AQ624891 CITBI-E1-
c	28	106	10.4	349	9	AW592873	AW592873 hg04d01.x
c	29	106	10.4	441	10	H63593	H63593 yr26c04.r1
	30	104.4	10.2	2843	11	AK014576	AK014576 Mus muscu
c	31	104.2	10.2	607	12	BH316806	BH316806 CH230-194
	32	104	10.2	423	12	AQ491155	AQ491155 RPCI-11-2
	33	103.6	10.2	584	12	AQ386543	AQ386543 RPCI11-15
	34	103.6	10.2	710	12	AQ351848	AQ351848 CITBI-E1-
	35	103.2	10.1	570	9	AW954120	AW954120 EST366190
	36	102.8	10.1	530	12	AQ462403	AQ462403 HS_5130_A
c	37	101.6	10.0	623	9	AW894443	AW894443 CM2-NN003
c	38	100.8	9.9	507	12	AQ537983	AQ537983 RPCI-11-3
	39	100.2	9.8	594	10	BI961215	BI961215 MONO1_7_E
c	40	99.8	9.8	460	10	BF766876	BF766876 PM2-CS002
c	41	99.8	9.8	487	9	AU155269	AU155269 AU155269
c	42	99.8	9.8	583	12	AQ263967	AQ263967 CITBI-E1-
	43	99.6	9.8	447	9	AA194142	AA194142 zr37g03.r
c	44	99.6	9.8	467	12	AQ062337	AQ062337 CIT-HSP-2
	45	99.6	9.8	651	12	AG151628	AG151628 Pan trogl

ALIGNMENTS

RESULT 1
AY026753
LOCUS AY026753 900 bp mRNA linear HTC 13-JUL-2001
DEFINITION Homo sapiens interleukin-1 receptor antagonist FKSG75 (FKSG75) mRNA, complete cds.
ACCESSION AY026753
VERSION AY026753.1 GI:12829965
KEYWORDS HTC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS Wang,Y.-g., Li,T. and Gong,L.
TITLE Identification and characterization of FKSG75, a novel member of the interleukin-1 family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 900)
AUTHORS Wang,Y.-g.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2001) Beijing FENGKESHENG Function Gene Technology Ltd., 4 Tou Tiao Lu Chang Street, Xuanwu District, Beijing 100050, P.R.China
FEATURES Location/Qualifiers
source 1. .900
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p14"
gene 1. .900
/gene="FKSG75"
CDS 91. .525
/gene="FKSG75"
/note="similar to IL1RN and IL1HY1"
/codon_start=1
/product="interleukin-1 receptor antagonist FKSG75"
/protein_id="AAK01948.1"
/db_xref="GI:12829966"
/translation="MSSSFLPEPLPAKSLQHGVPLSLDSSLSSLLEKICILPNRGLAR
TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAF

RLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQSW"
BASE COUNT 212 a 232 c 247 g 209 t
ORIGIN

Query Match 70.1%; Score 714.8; DB 11; Length 900;
Best Local Similarity 99.7%; Pred. No. 1.1e-166;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy    180 agagaagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcct 239
          ||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db    183 AGAGAAGATCTGCATACTTCCTAACAGAGGCTTGGCCCGCACCAAGGTCCCCATTTTCCT 242

Qy    240 ggggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccct 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GGGGATCCAGGGAGGGAGCCGCTGCCTGGCATGTGTGGAGACAGAAGAGGGGCCTTCCCT 302

Qy    300 acagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgctt 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 ACAGCTGGAGGATGTGAACATTGAGGAACTGTACAAAGGTGGTGAAGAGGCCACACGCTT 362

Qy    360 caccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctgg 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 CACCTTCTTCCAGAGCAGCTCAGGCTCCGCCTTCAGGCTTGAGGCTGCTGCCTGGCCTGG 422

Qy    420 ctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtga 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 CTGGTTCCTGTGTGGCCCGGCAGAGCCCCAGCAGCCAGTACAGCTCACCAAGGAGAGTGA 482

Qy    480 gccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcg 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 GCCCTCAGCCCGTACCAAGTTTTACTTTGAACAGAGCTGGTAGGGAGACAGGAAACTGCG 542

Qy    540 ttttagccttgtgccccccaaaccaagctcatcctgctcagggtctatggtaggcagaata 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 TTTTAGCCTTGTGCCCCCAAACCAAGCTCATCCTGCTCAGGGTCTATGGTAGGCAGAATA 602

Qy    600 atgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacat 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 ATGTCCCCCGAAATATGTCCACATCCTAATCCCAAGATCTGTGCATATGTTACCATACAT 662

Qy    660 gtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcct 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 GTCCAAAGAGGTTTTGCAAATGTGATTATGTTAAGGATCTTGAAATGAGGAGACAATCCT 722

Qy    720 gggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagaga 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      723 GGGTTATCCTTGTGGGCTCAGTTTAATCACAAGAAGGAGGCAGGAAGGGAGAGTCAGAGA 782

Qy    780 gagaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaaca 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    783 GAGAATGGAAGATACCATGCTTCTAATTTTGAAGATGGAGTGAGGGGCCTTGAGCCAACA 842

Qy    840 aatgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtct 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    843 AATGCAGGTGTTTTTAGAAGGTGGAAAAGCCAAGGGAACGGATTCTCCTCTAGAGTCT 900
```

RESULT 2
BI051175/c
LOCUS BI051175 285 bp mRNA linear EST 15-JUN-2001
DEFINITION CM2-GN0289-100101-685-c09 GN0289 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI051175
VERSION BI051175.1 GI:14458705
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 285)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL *Proc. Natl. Acad. Sci. U.S.A.* 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the *FAPESP/LICR Human Cancer Genome* Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM2&t2=CM2-GN0289-*100101-685-c09*&t3=2001-01-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 285.
FEATURES Location/Qualifiers
source 1. .285
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0289"
/dev_stage="Adult"
/note="Organ: placenta_normal; *Vector: puc18*; Site_1: SmaI ; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 58 a 85 c 78 g 64 t
ORIGIN

Query Match 24.5%; Score 250.2; DB 10; Length 285;
Best Local Similarity 96.5%; Pred. No. 1.6e-51;
Matches 277; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

```
Qy    273 tgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaactgta 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 TGTGGAGACAGAAGAGGGGCCTTCCCTACAGCTGGAGGATGTGAACATTGAGGAACTGTA 226

Qy    333 caaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgcctt 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CAAAGGTGGTGAAGAGGCCACACGCTTCACCTTCTTCCAGAGCAGCTCAGGCTCCGCCTT 166

Qy    393 caggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagccccagca 452
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    165 CAGGCTTGAGGCTGCTGCCTGGCCT-GCTGGTTCCTGTGTGGCCCGGCAGAGCCCCAGCA 107

Qy    453 gccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttactttgaaca 512
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    106 GCCAGTACAGCTCACCAAGGAGAGTGAGCCCTCAGCCCGTACCAAGTTTTACTTTGGACA 47

Qy    513 gagctggtagggagacaggaaactgcgttttagccttgtgcccccaa 559
          ||||| |||||||||||||||||||||||| | |    |||| |
Db     46 GAGCT-GTAGGGAGACAGGAAACTGCGTTTTAGACATTGTGCCCCCA 1
```

RESULT 3
AQ766579/c
LOCUS AQ766579 589 bp DNA linear GSS 28-JUL-1999
DEFINITION *HS_2192_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo* sapiens genomic clone Plate=2192 Col=17 Row=J, DNA sequence.
ACCESSION AQ766579
VERSION AQ766579.1 GI:5644695
KEYWORDS GSS.
SOURCE human.

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 2192  row: J  column: 17
            Seq primer: M13 Reverse
            Class: BAC ends
            High quality sequence stop: 589.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=2192 Col=17 Row=J"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT      152 a    147 c    100 g    135 t     55 others
ORIGIN
```

```
  Query Match             23.9%;  Score 244.2;  DB 12;  Length 589;
  Best Local Similarity   87.3%;  Pred. No. 5.3e-50;
  Matches  267;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy    703 aatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaagaaggaggcag 762
          |||||||||||| ||| ||||| ||| |||||||||||||||||||||||| |  |||||||
Db    586 AATGAGGAGACTATCGTGGGTAATCTTTGTGGGCTCAGTTTAATCACAAAAGTGAGGCAG 527

Qy    763 gaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatggagtga 822
          ||||||||||||||| ||||||||| ||||| ||||| |||||||||||||||||||| ||
Db    526 GAAGGGAGAGTCAGACAGAGAATGCAAGATCCCATGATTCTAATTTTGAAGATGGAGGGA 467

Qy    823 ggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaagggaacggat 882
          ||||| ||    || ||| |||||||||||||||||||||||||||||| || |||||
Db    466 GGGGCATTAGCTCACCAAGTGCAGGTGTTTTTAGAAGGTGGAAAAGCCAAGTGACCGGAT 407

Qy    883 tctcctctagagtctccggaaggaacacagctcttgacacatggatttcagctcagtgac 942
          |||| ||||||||||| |||||||||| |||||||||||||||||||||| ||||||||||
Db    406 TCTCTTCTAGAGTCTCTGGAAGGAACTCAGCTCTTGACACATGGATTTCGGCTCAGTGAC 347

Qy    943 acccatttcagacttctgacctccacaactataaaataataaacttgtgttattgtaaac 1002
           ||||||||  | || |||||||||| | |||| |||||| || |||||||||| |||  |
Db    346 NCCCATTTCGTATTTTTGACCTCCACGAATATAGAATAATGAATTTGTGTTATGGTACCC 287

Qy   1003 ctctaa 1008
          ||||||
Db    286 ATCTAA 281


RESULT   4
BE067002
LOCUS       BE067002                 574 bp    mRNA    linear   EST 09-JUN-2000
DEFINITION  PM0-BT0340-170100-004-b01 BT0340 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE067002
VERSION     BE067002.1  GI:8411652
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 574)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM0-BT0340-170
            100-004-b01&t3=2000-01-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 573.
FEATURES             Location/Qualifiers
     source          1. .574
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT0340"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      144 a    111 c    154 g    165 t
ORIGIN
```

```
  Query Match             16.5%;  Score 168.6;  DB 9;  Length 574;
  Best Local Similarity   68.1%;  Pred. No. 2.9e-31;
  Matches  280;  Conservative    0;  Mismatches  124;  Indels    7;  Gaps    3;

Qy    603 tcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtc 662
          | |||| |||  ||||||  ||||||||     | |||||  |||||||||  ||  || | |
Db     55 TACCCCCAAAGGTGTCCATGTCCTAATCTTGGAACCTGTGGATATGTTACATTATGTGGC 114

Qy    663 caaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctggg 722
           || ||| |||||||  ||||||||  |  || ||||||||  ||| |||||   |||||
Db    115 AAAGGAGATTTTGCATGTGTGATTAAGGGAAAGATCTTGAGATGGGGAGATTCTCCTGCA 174

Qy    723 ttatccttgtgggctcagtttaatcacaagaa----ggaggcaggaagggagagtcagag 778
          | | ||  || ||| || | |||| |||||  |       |   |||||||  ||      |
Db    175 TGACCCAGGTAGGCCCAATGTAATTACAAGGATCTTTAAAAGAGGAAGGTAGGAGGTCAC 234

Qy    779 agagaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaac 838
          ||  |  |  ||| | || | ||||   |||||||  |||||  |||||||   ||||||
Db    235 AGTCAGGGAGAGAGAGCAGGATTCTGGCTTTGAAGGTGGAGGAAGGGGCCACAAGCCAAG 294

Qy    839 aaatgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctc 898
          ||||||||||    |    || ||| |||| ||| ||   |||||| ||  | ||| |||
Db    295 AAATGCAGGTGGCCTCTAGAGCTGGGAAAGGCAATGG-GTGGATTCCCCCTTGGAGCCTC 353

Qy    899 cggaaggaacacagctct--tgacacatggatttcagctcagtgacacccatttcagact 956
          | ||||||||||||| ||  |||| | | | | | ||| ||| || |||| |||  ||
Db    354 CAGAAGGAACACAGCCCTGCTGACTCCTTGGTCTTAGCCCAGCGAGACCCGTTTTGGAAA 413
```

```
Qy    957 tctgacctccacaactataaaataataaacttgtgttattgtaaacctcta 1007
          || ||||| || || |  || ||  |||| ||||||| |||||| || |||
Db    414 TCAGACCTGCATAATTGCAAGATGGTAAATTTGTGTTGTTGTAAGCCACTA 464


RESULT   5
AI889529/c
LOCUS       AI889529                 507 bp    mRNA    linear   EST 01-SEP-1999
DEFINITION  wn05g02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2444594 3'
            similar to contains MER26.t1 MER26 repetitive element ;, mRNA
            sequence.
ACCESSION   AI889529
VERSION     AI889529.1  GI:5594693
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 407.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2444594"
                     /clone_lib="NCI_CGAP_Ut1"
                     /tissue_type="well-differentiated endometrial
                     adenocarcinoma, 7 pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Life Technologies catalog #:
                     11538-014"
BASE COUNT      127 a    136 c     98 g    146 t
ORIGIN


  Query Match             13.5%;  Score 137.2;  DB 9;  Length 507;
  Best Local Similarity   64.5%;  Pred. No. 1.8e-23;
  Matches  272;  Conservative    0;  Mismatches  138;  Indels   12;  Gaps    4;

Qy    587 ggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgcata 646
          ||| | |||||| ||| ||||| ||      |     | || ||     || | | |||
Db    418 GGTGGACAGAATCATGGCCCCCAAAGATGTCCATGTCCTAAACCCTGGATTCAGCGAATA 359

Qy    647 tgttaccatacatgtccaaagaggttttgcaaatgtgattatg---ttaaggatcttgaa 703
          ||||||| |||||| | |||| || ||| |  ||| | ||| |   || | |||   |||
Db    358 TGTTACCTTACATGACAAAAGGGGCTTTACTGATGCGCTTAAGGATTTTAAGATACGGAA 299

Qy    704 atgaggagacaatcctgggttatccttgtgggctcagtttaatcacaagaaggaggcagg 763
          ||           ||   |         ||| ||  | |||   ||| | |||||||||
Db    298 ATTGTCCAGGTGGGCTCAATGTAATCACAGGGGTCTTTATAAAAGCAAAAGGGAGGCAGG 239

Qy    764 aagggagagtcagagagagaatggaagataccatgcttctaattttgaagatggagtgag 823
          |||     |||||||||||  | |||||| | | | |  | | ||||||||||||||  ||
Db    238 AAG-----GTCAGAGAGAGGTTTGAAGATGCTACGTTATTGACTTTGAAGATGGAGGAAG 184
```

```
Qy    824 gggccttgagccaacaaatgcaggt-gtttttagaaggtggaaaagccaagggaacggat 882
          | ||| ||||||||  |||| |||| || | ||| || |||||||| ||||| || |  |
Db    183 GAGCCATGAGCCAAGGAATGTAGGTGGTGTCTAGGAGCTGGAAAAGTCAAGGTAATGAGT 124

Qy    883 tctcctctagagtctccggaaggaacacagctcttgacaca---tggatttcagctcagt 939
          | ||   |||||||||| ||| | ||  | | ||    |||   | ||||| | |  | |
Db    123 TGTCTCTTAGAGTCTCCTGAATGGACGAAACCCTGTCAACAACCTTGATTTTAACCAAAT 64

Qy    940 gacacccatttcagacttctgacctccacaactataaaataataaacttgtgttattgta 999
          || |||||||  |||||||||||||| |||| | | |||||  ||  || || ||
Db     63 GAGACCCATTTTGGACTTCTGACCTCCAGAACTGTGAGAGAATAAATGTGCTTTGTTTTA 4

Qy   1000 aa 1001
          ||
Db      3 AA 2


RESULT   6
AI393136/c
LOCUS       AI393136                 459 bp    mRNA    linear   EST 30-MAR-1999
DEFINITION  tg41c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2111348 3', mRNA sequence.
ACCESSION   AI393136
VERSION     AI393136.1  GI:4222683
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1519   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2111348"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
BASE COUNT      121 a    113 c     86 g    138 t      1 others
ORIGIN


  Query Match             12.5%;  Score 128;  DB 9;  Length 459;
  Best Local Similarity   61.2%;  Pred. No. 3.3e-21;
  Matches  270;  Conservative    0;  Mismatches  146;  Indels   25;  Gaps    3;

Qy    563 aagctcatcctgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccaca 622
          ||| | |     || |  |     | ||||| || ||||| | |||  || |||||||| |
Db    418 AAGATAAAANAACTGACCGAAGGAGATAGGCTGAGTAATGGCTCCCTCAAGATGTCCATA 359

Qy    623 tcctaatcccaagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgt 682
```

```
Db    358 TTTCATCCCTGGAACCTGTGAATACATTTCTTTATGTGGCAAAAGGGACTTTGTGGCTGT 299

Qy    683 gattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtgggctcagtt 742
Db    298 GATTAAACTAAGAACCTTGAAATGAGGAGATTCTCCGGGATCGTCCAGATGCATCAAATG 239

Qy    743 taatcacaagaaggaggcaggaagggagagtcagagagagaatggaagataccatgcttc 802
Db    238 TAACAAGAAG----------------GAGTCAGAGTCAGGCTGGAAGCCGCTATGCTGC 196

Qy    803 taattttgaagatggagtgaggggccttgagccaacaaatgcaggtgtttttagaaggtg 862
Db    195 TGGCTTTGAAGGCAGATGAAGGGGC------CAAGGAATTAGGGTGGTCTCTAGAATCTG 142

Qy    863 gaaaagccaagggaacggattctcctctagagtctccggaaggaacacagc--tcttgac 920
Db    141 GAAAAGGCAATGAAATTGATTCTCCCCTAGAGCTTTCAGAAGGAATGCAGCCTTGCCCAC 82

Qy    921 acatggatttcagctcagtgacacccatttcagacttctgacctccacaactataaaata 980
Db     81 ACCTTCATTTTAGACCAGTGAAACTGATTTTAGACTTCTGACTGCCAGAACTGTAAGATA 22

Qy    981 ataaacttgtgttattgtaaa 1001
Db     21 ATAAATGTATATTGATTGAAA 1
```

RESULT 7
AA417044/c
LOCUS AA417044 392 bp mRNA linear EST 09-NOV-1997
DEFINITION zu13d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731715 3', mRNA sequence.
ACCESSION AA417044
VERSION AA417044.1 GI:2077170
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 392)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 715 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 254.
FEATURES Location/Qualifiers
source 1. .392
/organism="Homo sapiens"
/db_xref="GDB:5928790"
/db_xref="taxon:9606"
/clone="IMAGE:731715"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories , Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 96 a 99 c 66 g 131 t
ORIGIN

Query Match 12.5%; Score 127.4; DB 9; Length 392;
Best Local Similarity 65.0%; Pred. No. 4.6e-21;
Matches 258; Conservative 0; Mismatches 121; Indels 18; Gaps 4;

```
Qy    617 tccacatcctaatccc-aagatctgtgcatatgttaccatacatgtccaaagaggttttg 675
Db    392 TCCACATCCTAATCCCTGGGACCTATGAATATGTTACCTTACATGGTAAAAGGGATTTTG 333

Qy    676 caaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtggg 735
Db    332 CAGATGTGAGTAAATGAAGACTCTTGATATGAGGAGATTACCTTGGATTATCCATGTGGA 273

Qy    736 ctc----agtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaaga 791
Db    272 CCCGAGGATATCTATGAGGGAAAGAGGGATGCAGGAGAGTCAGAGTCGGAAAAAGGAATG 213

Qy    792 taccatgcttctaattttgaagatggagtgagg-----ggccttgagccaacaaatgcag 846
Db    212 TTCAAGGAAAGCAGAGGTCAGAGTGATGTGAAGATCCTGGCTTTGAAGATGGACTGCAAG 153

Qy    847 gtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaagga 906
Db    152 TGGTTTGTAAAAACTGGAAAGGGCAAAGAAATTAATTCTCCCCTAGAACCTGCAGAAGAA 93

Qy    907 acacagctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctcc 966
Db     92 ACACAGACCTTGAC--------TTTAGCCCAGTAAGACCCATTTGGGACCTCTGACCTCC 41

Qy    967 acaactataaaataataaacttgtgttattgtaaacc 1003
Db     40 AGAACTGTAAGATAATAAATTAGTGTTGTTTTAAGCC 4
```

RESULT 8
AQ780593/c
LOCUS AQ780593 718 bp DNA linear GSS 02-AUG-1999
DEFINITION HS_3138_A1_B02_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138 Col=3 Row=C, DNA sequence.
ACCESSION AQ780593
VERSION AQ780593.1 GI:5683553
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3138 row: C column: 3
Seq primer: T7
Class: BAC ends

```
          High quality sequence stop: 718.
FEATURES             Location/Qualifiers
     source          1. .718
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=3138 Col=3 Row=C"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT      176 a    173 c    151 g    217 t      1 others
ORIGIN
```

```
  Query Match            12.4%;  Score 126.2;  DB 12;  Length 718;
  Best Local Similarity   62.1%;  Pred. No. 9.8e-21;
  Matches  239;  Conservative    0;  Mismatches  133;  Indels   13;  Gaps    2;

Db    649 ttaccatacatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgag 708
          |||    | |||   |||||| |||||||||||||||||| || |||||||| ||||| |
Db    718 TTAGGTCAAATGCGAAAAGAGATTTTGCAAATGTGATTAAGTCAAGGATCTTAAAATGGG 659

Qy    709 gagacaatcctgggttatccttgt----------gggctcagtttaatcacaagaagga 757
          | |  | |||| |   ||  |           || |       ||     |||||||
Db    658 GCAATTACTCTGGATATCCCCCATGAAATTGCAAGGGTCCATCAAAAAGTCAGAGAAGGA 599

Qy    758 ggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatgg 817
          ||  ||   | |  |||||||||||  || ||| |   || ||    |||||| |||
Db    598 GGTGTGACCATAAAACCAGAGAGAGAGGTGAGGATGCTGCACTGCTGGCCTTGAAGGTGG 539

Qy    818 agtgaggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaagggaa 877
          ||  ||||||   |||  |   |||||||     |     |    | |||    | ||||
Db    538 AGGACGGGGCCACAAGCAGAGGCATGCAGGCTGCCTCTAGAAACTGGAAAAGGCAAGGAA 479

Qy    878 cggattctcctctagagtctccggaaggaacacagctct--tgacacatggatttcagct 935
           ||||||||||||||||  ||| |||||||  | || ||  ||||||  | |  ||| | |
Db    478 TGGATTCTCCTCTAGAGCTTCCAGAAGGAAAGCGGCCCTGCTGACACCTTGGTTTTAACC 419

Qy    936 cagtgacacccatttcagacttctgacctccacaactataaaatataaaacttgtgttat 995
          ||||||||||||||| |||||||| |||| | ||| | || ||||| |     ||||
Db    418 CAGTGACACCCATTTTAGACTTCTGTCCTCTAGAACCACAAGATAATCATTGCATGTTGC 359

Qy    996 tgtaaacctctaaaaaaaaaaaaaa 1020
          | | | || |||||     | ||||
Db    358 TTTGAGCCACTAAATTTGTAGAAAA 334
```

```
RESULT  9
AQ356956/c
LOCUS       AQ356956                612 bp    DNA     linear   GSS 24-JAN-1999
DEFINITION  CITBI-E1-2529E8.TR CITBI-E1 Homo sapiens genomic clone 2529E8, DNA
            sequence.
ACCESSION   AQ356956
VERSION     AQ356956.1  GI:4184129
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2529E8.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .612
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2529E8"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT      156 a    139 c    126 g    191 t
ORIGIN
```

```
  Query Match            12.3%;  Score 125;  DB 12;  Length 612;
  Best Local Similarity   64.2%;  Pred. No. 1.9e-20;
  Matches  296;  Conservative    0;  Mismatches  135;  Indels   30;  Gaps    6;

Qy    559 aaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccgaaatatgtc 618
          || ||| |  || | |  ||  |||  || ||| ||||||||     ||| ||| |||||
Db    529 AAACAATCAGATGCAGACCAATGTCACTGTTAGACAGAATAACAGATCCCCAAAGATGTC 470

Qy    619 cacatcctaatcccaagat-ctgtgcatatgttaccatacatgtccaaagaggttttgca 677
          |||||||||||||| |||  ||||  |||||| | | |||||| | |||||   ||||||
Db    469 CACATCCTAATCCCCAGAACCTGTAAATATGTCATCCTACATGGCAAAAGACACTTTGCA 410

Qy    678 aatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtgggct 737
          | || |     ||| | ||||||| |||  | ||  || |||| ||| ||  ||| |||
Db    409 GACGTCA-----TTAGGAATCTTGAGATGGTGGGATTATGCTGGATTACCCAGGTGAGCT 355

Qy    738 cagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaagataccat 797
          |||  |  | | ||    ||   | || |   |||    | || || | || |  || |
Db    354 CAGCGTCTTTAAAAATGAGACAGA-GAGGCAGGAGAGTCAAAGTGATTTGATGTGACGAG 296

Qy    798 gcttcta--------------attttgaagatggagtgaggggccttgagccaacaaatg 843
          |  || |               |||  | | ||| |   ||| || |||| |||  ||||
Db    295 GACTCAACCTGCGGTTGCTGGCTTTGAAGGCTGGGGAAGGGGACCATGAGTCAAGGAATG 236

Qy    844 caggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaa 903
          |  |  | ||||| ||||||||    |  ||| |||||||| |||| | ||||||||
Db    235 TGGCAGCCTCTAGAAGCTGGAAAAGGAGGGCAAACAGATTCTCCCCTAGGGCCTCCGGAA 176

Qy    904 ggaacacagctcttgacacatggatttcagctcagtgacacccatttcagacttctgacc 963
          |  |      |  | | ||||| ||| |||||| |||||||  ||||||||||
Db    175 GAGA--------TGCAATCTTTGATTTTAGCCCAGTGAAACCCATTTGGGACTTCTGACC 124

Qy    964 tccacaact-ataaaatataaacttgtgttattgtaaacc 1003
          |||| |||| |||| |||||||  |||||||  || ||| ||
Db    123 TCCAGAACTAATAAGATAATAAGTTTGTGTTGTTTTAAGCC 83
```

```
RESULT  10
AQ442721
LOCUS       AQ442721                533 bp    DNA     linear   GSS 31-MAR-1999
DEFINITION  HS_5116_B2_G04_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=692 Col=8 Row=N, DNA sequence.
ACCESSION   AQ442721
VERSION     AQ442721.1  GI:4554060
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
```

```
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 692  row: N  column: 8
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 533.
FEATURES             Location/Qualifiers
     source          1. .533
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=692 Col=8 Row=N"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT      178 a     98 c    115 g    135 t      7 others
ORIGIN
```

```
  Query Match             12.0%;  Score 122.2;  DB 12;  Length 533;
  Best Local Similarity   64.4%;  Pred. No. 9.3e-20;
  Matches  269;  Conservative    0;  Mismatches  129;  Indels   20;  Gaps    5;

Qy     561 ccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccgaaatatgtcca 620
           | |  ||| |    ||     | | |||||| |||||||||    |  || |||  |
Db     117 CAAGACTCCTTGCTCTATACTTTTGTGGTAGAGAGAATAATGATTTCTCAAGTAT-CCAT 175

Qy     621 catcctaatcccaagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaat 680
           | |  |  ||||    ||||| |||| ||||| | |||| | |||| |  ||| || ||
Db     176 GACCGAATACCCAGAGCCTGTGAATATATTACCTTCCATGGCAAAAGGGACTTTACAGAT 235

Qy     681 gtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtgggctcag 740
           |||||||  |||||||||||||| |||||| ||  | ||||| ||  ||  |||||| |||
Db     236 GTGATTAACTTAAGGATCTTGACATGAGG-GATTAACCTGGATTTGCCAGGTGGGCCCAG 294

Qy     741 tttaatcacaagaaggaggcag----------gaagggagagtcagagagagaatgg 787
           | ||||||||||||      ||           ||  |||||||||||| ||| | |
Db     295 TATAATCACAAGAATACTTAAGAATGGAAGAGGCAGACAGGAGAGTCAGAGAAAGATTTG 354

Qy     788 aagataccatgcttctaatttttgaagatggagtgaggggccttgagccaacaaatgca-g 846
           ||| | | |  |  ||   |||||| || |||  ||||||  |||||||  | ||||
Db     355 AAGGTGCTACACCACTGGCTTTGAAAATAGAGGAAGGGGCTGTGAGCCAAGGAGTGCACA 414

Qy     847 gtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaa--- 903
           ||  ||||  || ||| |||  ||| | |||  ||||||||||| ||| ||| |||
Db     415 CTGCCTTTATGAGCTGGCAAAAACAAAGAAACAAATTCTCCTCTATAGTTTCCAGAAAAC 474

Qy     904 -ggaacacagctcttgacacatggatttcagctcagtgacacccatttcagacttctg 960
            |||  ||| |||||| | ||||  ||| ||||   |  | |||   |||||||
Db     475 GAACACAACCCTCCTGACACCTTGATTNTAGCCCAGTAGAAATCCTTTTGCACTTCTG 532
```

```
RESULT  11
AQ318555
LOCUS       AQ318555               526 bp    DNA     linear   GSS 04-MAY-1999
DEFINITION  RPCI11-90J12.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-90J12,
            DNA sequence.
ACCESSION   AQ318555
VERSION     AQ318555.1  GI:4051597
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  TITLE     Use of human BAC End Sequences for Sequence-Ready Map Building
  JOURNAL   Unpublished (1998)
COMMENT     Other_GSSs: RPCI11-90J12.TV
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /db_xref="GDB:7534403"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-90J12"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      158 a     86 c    122 g    160 t
ORIGIN
```

```
  Query Match             11.9%;  Score 121;  DB 12;  Length 526;
  Best Local Similarity   59.3%;  Pred. No. 1.8e-19;
  Matches  246;  Conservative    0;  Mismatches  160;  Indels    9;  Gaps    2;

Qy     583 ctatggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaag-atctgt 641
           |||||||| || ||||||||  |  |  || | |||| ||| || |||||  | ||||||
Db      56 CTATGGTAAGCGGAATAATGGACTTCCCAAAAGGTCCTCATTCTCATCCCTGGAATCTGT 115

Qy     642 gcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaaggatcttg 701
           | |||||||||  ||||||   |||| |  ||| || |||||||||  ||||||||||||
Db     116 GAATATGTTACTTTACATGGTAAAAGGGACTTTACAGATGTGATTAAGTTAAGGATCTTG 175

Qy     702 aaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaagaaggaggca 761
           | ||| |||||   | |||| ||||     |  | | |  |  ||  ||       |
Db     176 AGATGTGGAGATTCTTCTGGATTATTTGCATACACGAAATAAACACAAGAGTCATGATAA 235

Qy     762 ggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatggagtg 821
           |  |  |  |  | |  ||   |    || ||     |  |  ||||   ||       |
Db     236 GAGATAGGTACTAGGATTAAAGTCGGTAGTAGGAAATATGATAATAGAGA--------TT 287

Qy     822 aggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaagggaacgga 881
           | |   | ||||     | ||| ||     ||   | |  || | ||  | |||||  |
Db     288 GGTGTAATGGAGCTGTGGAGTGCTGGCAGCCTTTAGAAGCTGAGAGGCGCAAGGAACAGG 347

Qy     882 ttctcctctagagtctccggaaggaacacagctcttgacacatggatttcagctcagtga 941
           || ||| || || |||| | |||||||        |||||  | |||||  || |  | |
Db     348 TTTTCCCCTGGAATCTCTGAAAGGAACCAGCTCGCTGACATCTTGATTTTGGCCCCATAA 407

Qy     942 cacccatttcagacttctgacctccacaactataaaataataaacttgtgttatt 996
```

```
Db    408 GATTCATTTTGAACTTCTGACCTCCAAGACCATAAGAGAATAACTGTATGTTTTT 462


RESULT  12
AA447609/c
LOCUS       AA447609                375 bp    mRNA    linear   EST 04-JUN-1997
DEFINITION  zw82d06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782699
            3', mRNA sequence.
ACCESSION   AA447609
VERSION     AA447609.1  GI:2161279
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 322.
FEATURES             Location/Qualifiers
     source          1. .375
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:782699"
                     /clone_lib="Soares_testis_NHT"
                     /sex="male"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech Laboratories
                     , Inc., and primed with  a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      102 a    90 c    72 g    111 t
ORIGIN


  Query Match             11.4%;  Score 116.6;  DB 9;  Length 375;
  Best Local Similarity   62.3%;  Pred. No. 2.2e-18;
  Matches  246;  Conservative    0;  Mismatches  124;  Indels   25;  Gaps    3;

Qy    604 cccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtcc 663
          | |||  || ||||||| ||   |  ||    | ||||| |||  || |  ||  || | |
Db    374 CTCCCTCAAGATGTCCATATTTCATCCCTGGAACCTGTGAATACATTTCTTTATGTGGCA 315

Qy    664 aaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggt 723
          |||| |  ||||    ||||||||   |||| | ||||||||||||||||   ||| || |
Db    314 AAAGGGACTTTGTGGCTGTGATTAAACTAAGAACCTTGAAATGAGGAGATTCTCCGGGAT 255

Qy    724 tatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagaga 783
            |||   ||     | | |||  | |||                 |||||||||  ||
Db    254 CGTCCAGATGCATCAAATGTAACAAGAAG----------------GAGTCAGAGTCAGG 212

Qy    784 atggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaacaaatg 843
          | ||||  | ||||| ||  |||||||  ||  ||||||     | |  || |
```

```
Db    211 CTAGAAGTCGCTATGCTGCTGGCTTTGAAGGCAGATGAAGGGGC------CAAGGAATTA 158

Qy    844 caggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaa 903
          |  || | |||||  |||||||| ||| | ||  |||||||| ||||||  | | |||
Db    157 GGGTGGTCTCTAGAATCTGGAAAAGGCAATGAAATTGATTCTCCCCTAGAGCTTTCAGAA 98

Qy    904 ggaacacagc--tcttgacacatggatttcagctcagtgacacccatttcagacttctga 961
          ||||  ||||  |    |||| |  |||| ||  |||||| ||  ||||||||||||||
Db     97 GGAATGCAGCCTTGCCCACACCTTCATTTTAGACCAGTGAAACTGATTTCAGACTTCTGA 38

Qy    962 cctccacaactataaaataataaacttgtgttatt 996
          |  ||| |||| ||| ||||||||  | | || ||
Db     37 CTGCCAGAACTGTAAGATAATAAATGTATATTGTT 3


RESULT  13
AG087298/c
LOCUS       AG087298                670 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-085013.R, genomic survey sequence.
ACCESSION   AG087298
VERSION     AG087298.1  GI:16639100
KEYWORDS    GSS; GSS (genome survey sequence).
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-085013.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (sites)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 670)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .670
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-085013.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      176 a    180 c    121 g    193 t
ORIGIN


  Query Match             11.4%;  Score 115.8;  DB 12;  Length 670;
  Best Local Similarity   64.2%;  Pred. No. 3.7e-18;
  Matches  228;  Conservative    0;  Mismatches  112;  Indels   15;  Gaps    3;

Qy    577 cagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaat-cccaag 635
          |||    | ||| ||||||||||||||   ||| | | |  | ||| ||| | | |
Db    526 CAGCTGGTCTGGGAGGCAGAATAATGGGTCCCCAGAAACATACACGTCCCATTGTCTGCA 467

Qy    636 atctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaagg 695
          | |||||    |||||||  || || |  | |    | |||| ||| ||||  || ||||
Db    466 ACCTGTGAGCCTGTTACCTCACGTGGCAGATGGTACTGTGCACATGGGATTGAGTGAAGG 407
```

```
Qy    696 atcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag--- 752
          ||||||| |||||||| |||||||  |  ||    ||       |  |||||||||
Db    406 ATCTTGAGATGAGGAGGTTATCCTGGATATTCTGGATGAATCTGATGCAATCACAAGGGT 347

Qy    753 ----------aaggaggcaggaagggagagtcagagagagaatggaagataccatgcttc 802
                   ||| |  |  |  | ||||||||||||| | ||||||||  |     |
Db    346 CCTTATAAGAAAGAGGCATGAGGGTCAGAGTCAGAGAGAAACTGGAAGATGGTACCTAGC 287

Qy    803 taattttgaagatggagtgaggggccttgagccaacaaatgcaggt-gtttttagaaggt 861
          |  |||||||| ||| |||||||  | ||||  |||||||| | || ||||||  |
Db    286 TGGCTTTGAAGATAGAGGAAGGGGCCAGAAACCAAGGAATGCAGGTGGCTTCTAGAAGCT 227

Qy    862 ggaaaagccaagggaacggattctcctctagagtctccggaaggaacacagctct 916
          ||||||| |||||||||   |||||| |||||| |||| |||||| ||   | ||
Db    226 GGAAAAGTCAAGGGAACTAGTTCTCCCCTAGAGCCTCCAGAAGGAGCATGACCCT 172
```

RESULT 14
B54722/c
LOCUS B54722 634 bp DNA linear GSS 20-JUN-1998
DEFINITION CIT-HSP-384F12.TR CIT-HSP Homo sapiens genomic clone 384F12, DNA sequence.
ACCESSION B54722
VERSION B54722.1 GI:2609056
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 634)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden ,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CIT-HSP-384F12.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .634
/organism="Homo sapiens"
/db_xref="GDB:5378290"
/db_xref="taxon:9606"
/clone="384F12"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT 161 a 154 c 118 g 201 t
ORIGIN

Query Match 11.3%; Score 115.4; DB 12; Length 634;
Best Local Similarity 60.9%; Pred. No. 4.6e-18;
Matches 282; Conservative 0; Mismatches 136; Indels 45; Gaps 4;

```
Qy    563 aagctcatcctgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccaca 622
          ||| | |  || |   |    | |||||||| | ||||     ||  ||| |||||||||
Db    579 AAGTTTAAGCTTCAGGGCTCTTGTGGTAGGCTGGATAACAGATCCTCAAAGATGTCCACA 520

Qy    623 tcctaatcccaag-------atctgtgcatatgttaccatacatgtccaaagaggttttg 675
          |||||||| ||         |||| || ||||||| |  | ||||   |||     ||||
Db    519 TCCTAATCCTAATCCCCAGAATCTATGAATATGTTGCTTTGCATGGTAAAAAGAACTTTG 460

Qy    676 caaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtggg 735
          |||||||||||| || || |||||||| ||  |||||  || |||| |||||  ||| |
Db    459 CAAATGTGATTAAGTGAAAGATCTTGAGATAGGGAGATTATTCTGGATTATCCAAGTGTG 400

Qy    736 ctcagtttaatcacaag-----------------------------------aaggagg 759
          | || | ||||||||||                                     |||
Db    399 CCCAATATAATCACAAGGGTCCTTATAAGGAGACAGGAGAGTCACAGAGGAAATGCAAGG 340

Qy    760 caggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatggag 819
            ||||   |||||||| |       ||    | |  || |||  ||||| ||||||
Db    339 ACAGAAGCAGAAGTCAGAGGGGTGTAAAAATGCTCTACACTGCTAGCTTTGAGGATGGAA 280

Qy    820 tgaggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaagggaacg 879
            ||| ||| |||||||   |     |  |  | ||| || |||| ||| || || |||
Db    279 AAAGGAGCCATGAGCCAGGGACGTAGGTGGCCTCTAGGAGCTGGAGAAGGCATGGCAACC 220

Qy    880 gattctcctctagagtctccggaaggaacacagctcttgacacatggatttcagctcagt 939
          | || |||  ||| |||||| |||||||  ||  ||  | ||| | ||||| |||||||
Db    219 AACTCCCCT-GAGAATCTCCAGAAGGAAAGCACTTCCCG-CACTTTGATTTTAGCTCAGC 162

Qy    940 gacacccatttcagacttctgacctccacaactataaaaataat 982
          || ||  |||| ||||||| |||||   |||| |||||||||
Db    161 GAAACTGATTTTGGACTTCTCACCTCTTGAACTGTAAAATAAT 119
```

RESULT 15
AQ405885/c
LOCUS AQ405885 525 bp DNA linear GSS 13-MAR-1999
DEFINITION HS_5043_B2_F07_T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=619 Col=14 Row=L, DNA sequence.
ACCESSION AQ405885
VERSION AQ405885.1 GI:4415873
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 619 row: L column: 14
Seq primer: T7
Class: BAC ends
High quality sequence stop: 525.
FEATURES Location/Qualifiers
source 1. .525
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=619 Col=14 Row=L"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 111 a 139 c 109 g 160 t 6 others
ORIGIN

Query Match 11.2%; Score 114.6; DB 12; Length 525;
Best Local Similarity 70.0%; Pred. No. 7.1e-18;
Matches 224; Conservative 0; Mismatches 90; Indels 6; Gaps 5;

```
Qy    636 atctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaagg 695
          | ||||  ||||||  ||| | |||| | |||||||  ||||| | |||||||   || |||
Db    361 ACCTGTCAATATGTGACCTTTCATGGCAAAAGAGACTTTGC-AGTGTGATTGGATTGAGG 303

Qy    696 atcttgaaatgaggagacaatcctgggttatcctt-gtgggctcagtttaatcacaagaa 754
          |||||||  |||||||||  |||  ||     |    ||   | |||       |  |||
Db    302 ATCTTGAGATGAGGAGATTATCTGGGTGGCCCTAAAGTAATCACAGGGGTCCTATGAGAC 243

Qy    755 ggaggcaggaaggg-agagtcagagagagaatggaagataccatgcttctaattttgaag 813
          ||||||||||  ||  |||||||  | |||||  ||||||||  |||  |||  |   |||||||
Db    242 GGAGGCAGGAGGGTCAGAGTCACACAGAGACTGGAAGATGCCACGCTGTTGGCTTTGAAG 183

Qy    814 atggagtgaggggccttgagccaacaaatgcagg-tgtttttagaaggtggaaaagccaa 872
            ||||   |||||||  ||||||||   |||||||  | ||  | |||  ||||||||  ||
Db    182 GTGGAAGAAGGGGCCATGAGCCAAGGCATGCAGGCAGCTTCCACAAGCTGGAAAAGGAAA 123

Qy    873 gggaacggattctcctctagagtctccggaaggaacacagctct--tgacacatggattt 930
          || ||| || ||||||||  |||  ||| ||||||||||| | ||  | | || | ||| |
Db    122 GGAAACAGACTCTCCTCTGGAGCATCCAGAAGGAACACAACCCTGCTAATACCTTGATNT 63

Qy    931 cagctcagtgacacccattt 950
            |||   |||| | ||||||
Db     62 TAGCCACGTGAGATCCATTT 43
```

Search completed: May 19, 2002, 08:44:01
Job time: 14234 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:52:07 ; Search time 11.75 Seconds
(without alignments)
474.302 Million cell updates/sec

Title: US-09-724-583-2
Perfect score: 818
Sequence: 1 MCSLPMARYYIIKYADQKAL.....QLTKESEPSARTKFYFEQSW 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	260.5	31.8	178	1	IL1X_RAT	P25086 rattus norv
2	257.5	31.5	178	1	IL1X_MOUSE	P25085 mus musculu
3	256	31.3	177	1	IL1X_PIG	Q29056 sus scrofa
4	241	29.5	177	1	IL1X_RABIT	P26890 oryctolagus
5	238.5	29.2	177	1	IL1X_HUMAN	P18510 homo sapien
6	238	29.1	177	1	IL1X_HORSE	O18999 equus cabal
7	232	28.4	174	1	IL1X_BOVIN	O77482 bos taurus
8	134.5	16.4	267	1	IL1B_PIG	P26889 sus scrofa
9	132	16.1	266	1	IL1B_SHEEP	P21621 ovis aries
10	124.5	15.2	269	1	IL1B_MOUSE	P10749 mus musculu
11	119.5	14.6	266	1	IL1B_CEREL	P51745 cervus elap
12	117	14.3	266	1	IL1B_BOVIN	P09428 bos taurus
13	112.5	13.8	268	1	IL1B_RAT	Q63264 rattus norv
14	111	13.6	266	1	IL1B_CAPHI	P79162 capra hircu
15	110.5	13.5	268	1	IL1B_RABIT	P14628 oryctolagus
16	106.5	13.0	268	1	IL1B_MACFA	P79182 macaca fasc
17	106.5	13.0	269	1	IL1B_CERTO	P46648 cercocebus
18	106.5	13.0	269	1	IL1B_MACMU	P48090 macaca mula
19	106.5	13.0	269	1	IL1B_MACNE	P51493 macaca neme
20	104.5	12.8	269	1	IL1B_HUMAN	P01584 homo sapien
21	94.5	11.6	267	1	IL1B_FELCA	P41687 felis silve
22	92	11.2	268	1	IL1B_HORSE	Q28386 equus cabal
23	77	9.4	997	1	YPX2_CAEEL	Q20256 caenorhabdi
24	76.5	9.4	520	1	CPF3_HUMAN	Q08477 homo sapien
25	71.5	8.7	4303	1	PKD1_HUMAN	P98161 homo sapien
26	71	8.7	2766	1	THYG_MOUSE	O08710 mus musculu
27	70.5	8.6	620	1	VLCS_MOUSE	O35488 mus musculu
28	70.5	8.6	827	1	GAG_IPMA	P11365 mouse intra
29	69.5	8.5	214	1	GTH7_ARATH	Q96324 arabidopsis
30	69	8.4	355	1	KLC3_HUMAN	Q9nsk0 homo sapien
31	69	8.4	520	1	CPF2_HUMAN	P78329 homo sapien
32	69	8.4	700	1	PURL_HALN1	Q9hr49 halobacteri
33	68.5	8.4	557	1	IGEB_MOUSE	P03975 mus musculu
34	67.5	8.3	271	1	IL1A_MACMU	P48089 macaca mula
35	67	8.2	665	1	Y176_METTH	O26278 methanobact
36	67	8.2	832	1	BGAL_ASPOF	P45582 asparagus o
37	66.5	8.1	271	1	IL1A_MACFA	P79340 macaca fasc
38	66.5	8.1	687	1	VS41_GIALA	P92127 giardia lam
39	66	8.1	254	1	TPIS_BUCAP	Q59179 buchnera ap
40	66	8.1	290	1	MAB3_CAEEL	O18214 caenorhabdi
41	66	8.1	438	1	GSA_STRCO	Q9f2s0 streptomyce
42	66	8.1	619	1	KLC3_MOUSE	Q9dbs5 mus musculu
43	65	7.9	531	1	G6PI_SYNY3	P52983 synechocyst
44	65	7.9	3206	1	POLG_PSBMV	P29152 p genome po
45	64.5	7.9	967	1	SYA_BOMMO	P21894 bombyx mori

ALIGNMENTS

RESULT 1
IL1X_RAT
ID IL1X_RAT STANDARD; PRT; 178 AA.
AC P25086;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL-1RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M63101; AAA41434.1; -.
DR PIR; C40956; C40956.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 92 142 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20282 MW; F3A5754FB6C51B03 CRC64;

Query Match 31.8%; Score 260.5; DB 1; Length 178;
Best Local Similarity 44.5%; Pred. No. 2.7e-20;
Matches 61; Conservative 16; Mismatches 53; Indels 7; Gaps 4;

Qy 16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74

```
          :||  | |: ||: |     |    |||  :|   :|   |  |||| ||  ||:||::
Db     45 NQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99

Qy     75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
          :   ||||:||| :| |  ||  |||| :| :|     |: | ||||||   |   || |
Db    100 DDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSL 159

Qy    135 TK-ESEPSARTKFYFEQ 150
          |    ||   |||||::
Db    160 TNTPKEPCTVTKFYFQE 176


RESULT   2
IL1X_MOUSE
ID   IL1X_MOUSE     STANDARD;      PRT;   178 AA.
AC   P25085;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL-1RA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91250712; PubMed=1828262;
RA   Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT   "Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT   gene mapping, and expression of mRNA in vitro and in vivo.";
RL   J. Immunol. 146:4228-4233(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91316273; PubMed=1830498;
RA   Matsushime H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT   "Cloning and expression of murine interleukin-1 receptor antagonist
RT   in macrophages stimulated by colony-stimulating factor 1.";
RL   Blood 78:616-623(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SWISS;
RX   MEDLINE=94271931; PubMed=8003626;
RA   Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
RT   "The mouse interleukin 1 receptor antagonist protein: gene structure
     and regulation in vitro.";
     Cytokine 6:1-9(1994).
     [4]
RP   SEQUENCE OF 7-178 FROM N.A.
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN   [5]
RP   SEQUENCE OF 23-178 FROM N.A.
RX   MEDLINE=92037824; PubMed=1834470;
RA   Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT   "Cloning, heterologous expression and characterization of murine
RT   interleukin 1 receptor antagonist protein.";
RL   Eur. J. Immunol. 21:2775-2780(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74294; AAA39309.1; -.
DR   EMBL; M64404; AAA39277.1; -.
DR   EMBL; L32838; AAA20576.1; -.
DR   EMBL; M57525; AAA39278.1; -.
DR   EMBL; M63100; AAA39310.1; -.
DR   EMBL; S64082; AAB20265.1; -.
DR   PIR; B40956; B40956.
DR   PIR; A44610; A44610.
DR   HSSP; P18510; 1IRA.
DR   MGD; MGI:96547; Il1rn.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID      92    142      BY SIMILARITY.
FT   CARBOHYD     110    110      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   178 AA;  20274 MW;  84AA002A3119C024 CRC64;


  Query Match             31.5%;  Score 257.5;  DB 1;  Length 178;
  Best Local Similarity   44.5%;  Pred. No. 5.5e-20;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy     16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
          :||  | |: ||: |     |    |||  :|   :|   |  |||| ||  ||:| ::
Db     45 NQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 99

Qy     75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
          :   ||||:||| :| |  ||  |||| :|  |     |:|| ||||||   |  :|| |
Db    100 DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 159

Qy    135 TK-ESEPSARTKFYFEQ 150
          |    ||   |||||::
Db    160 TNTPEEPLIVTKFYFQE 176


RESULT   3
IL1X_PIG
ID   IL1X_PIG       STANDARD;      PRT;   177 AA.
AC   Q29056;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IRAP1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CROSSBREED; TISSUE=Lung;
RA   Yin J., Murtaugh M.P.;
RT   "Characterization of IRAP in morphine treated pig.";
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; L38849; AAA99424.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20093 MW;  2114DC6119A9D5F9 CRC64;


  Query Match             31.3%;  Score 256;  DB 1;  Length 177;
  Best Local Similarity   40.5%;  Pred. No. 7.8e-20;
  Matches   62;  Conservative   21;  Mismatches   56;  Indels   14;  Gaps    5;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVP--IF 58
           |  :   | : :   :||  | |: ||: |     |    |||  :|        |  :|
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVPVE-------PHFVF 82

Qy      59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWP 118
           ||| ||  ||:||:: :   |||: ||| :| |  |:  |||| :| ||     |:|| |
Db      83 LGIHGGKLCLSCVKSGDEMKLQLDAVNITDLRKNSEQDKRFTFIRSDSGPTTSFESAACP 142

Qy     119 GWFLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||||   |  ||| ||   : : : |||||:|
Db     143 GWFLCTALEADQPVGLTNTPKAAVKVTKFYFQQ 175


RESULT   4
IL1X_RABIT
ID   IL1X_RABIT     STANDARD;      PRT;   177 AA.
AC   P26890;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
     SEQUENCE FROM N.A.
     MEDLINE=94165101; PubMed=7509813;
     Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA   Brewer M.T., Eisenberg S.P., Ng R.K.;
RT   "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT   functional characterization, and regulation during intestinal
RT   inflammation.";
RL   J. Biol. Chem. 269:6962-6971(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hamada H., Mulligan R.C.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93052512; PubMed=1427977;
RA   Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA   Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT   "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT   rabbits. Production, purification and determination of primary
RT   structure.";
RL   Immunology 77:235-244(1992).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; S68977; AAB30093.1; -.
DR   EMBL; M57526; AAA31374.1; -.
DR   EMBL; D21832; BAA04860.1; -.
DR   PIR; A54377; A54377.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20214 MW;  F5BC087F097FFEAF CRC64;


  Query Match             29.5%;  Score 241;  DB 1;  Length 177;
  Best Local Similarity   39.2%;  Pred. No. 2.9e-18;
  Matches   60;  Conservative   22;  Mismatches   57;  Indels   14;  Gaps    5;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVP--IF 58
           |  :   | : :   :||  | |: ||: |     |    |:|  :|         |  :|
Db      33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPLE-------PQLLF 82

Qy      59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWP 118
           |||| |  ||:||:: :   | || ||| :| |  |:  |||| :|:||     |:|: |
Db      83 LGIQRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCP 142

Qy     119 GWFLCGPAEPQQPVQLTKESEPS-ARTKFYFEQ 150
           |||||   |  ||| ||   : |   |||||::
Db     143 GWFLCTALEADQPVSLTNTPDDSIVVTKFYFQE 175


RESULT   5
IL1X_HUMAN
ID   IL1X_HUMAN     STANDARD;      PRT;   177 AA.
AC   P18510;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-
DE   1RA) (IRAP) (IL-1RN).
GN   IL1RN OR IL1RA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90220867; PubMed=2139180;
RA   Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA   Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA   Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,
RA   Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L.,
RA   Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;
RT   "Purification, cloning, expression and biological characterization of
RT   an interleukin-1 receptor antagonist protein.";
RL   Nature 344:633-638(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90136921; PubMed=2137201;
```

RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA Hannum C.H., Thompson R.C.;
RT "Primary structure and functional expression from complementary DNA
RT of a human interleukin-1 receptor antagonist.";
RL Nature 343:341-346(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92338323; PubMed=1385987;
RA Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
RA Sheer D., Solari R.;
RT "Cloning and chromosome mapping of the human interleukin-1 receptor
RT antagonist gene.";
RL Cytokine 4:83-89(1992).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97146044; PubMed=8992991;
RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA Arend W.P., Smith M.F. Jr.;
RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT and inducible regulatory regions.";
RL J. Immunol. 158:748-755(1997).
RN [6]
RP SEQUENCE OF 26-45.
RX MEDLINE=90136920; PubMed=2137200;
RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
RA Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
RT inhibitor.";
RL Nature 343:336-340(1990).
RN [7]
RP SEQUENCE OF 26-52.
RX MEDLINE=90354444; PubMed=2143761;
RA Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
RA Heinrikson R.L., Chosay J.G., Tracey D.E.;
RT "Purification and characterization of interleukin 1 receptor level
RT antagonist proteins from THP-1 cells.";
RL J. Biol. Chem. 265:14505-14511(1990).
[8]
SEQUENCE FROM N.A. (INTRACELLULAR FORM).
MEDLINE=91219436; PubMed=1827201;
RA Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT "cDNA cloning of an intracellular form of the human interleukin 1
RT receptor antagonist associated with epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN [9]
RP STRUCTURE BY NMR.
RX MEDLINE=92297633; PubMed=1534997;
RA Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT "Secondary structure and topology of interleukin-1 receptor
RT antagonist protein determined by heteronuclear three-dimensional NMR
RT spectroscopy.";
RL Biochemistry 31:5237-5244(1992).
RN [10]
RP STRUCTURE BY NMR.
RX MEDLINE=94320651; PubMed=8045306;
RA Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
RA Yem A.W., Deibel M.R. Jr.;
RT "Solution structure of human interleukin-1 receptor antagonist
RT protein.";
RL FEBS Lett. 349:79-83(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=94230368; PubMed=8175703;
RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
RA Brandhuber B.J.;
RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
RT resolution.";
RL J. Biol. Chem. 269:12874-12879(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=95172072; PubMed=7867645;
RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT "Refined crystal structure of the interleukin-1 receptor antagonist.
RT Presence of a disulfide link and a cis-proline.";
RL Eur. J. Biochem. 227:838-847(1995).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
RX MEDLINE=97215904; PubMed=9062194;
RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT "A new cytokine-receptor binding mode revealed by the crystal
RT structure of the IL-1 receptor with an antagonist.";
RL Nature 386:194-200(1997).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
CC FORM).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
CC PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -!- DATABASE: NAME=R&D Systems' cytokine source book;
CC WWW="http://www.rndsystems.com/cyt_cat/il1ra.html".
CC ---

CC ---
DR EMBL; M55646; AAA59138.1; -.
DR EMBL; M63099; AAB41943.1; -.
DR EMBL; X52015; CAA36262.1; -.
DR EMBL; X53296; CAA37386.1; -.
DR EMBL; X64532; CAA45832.1; -.
DR EMBL; U65590; AAB92268.1; -.
DR EMBL; U65590; AAB92270.1; -.
DR PIR; A30368; A30368.
DR PIR; A37822; A37822.
DR PIR; S08160; S08160.
DR PIR; S08159; S08159.
DR PIR; A40956; A40956.
DR PIR; A39386; A39386.
DR PDB; 1ITN; 30-APR-94.
DR PDB; 2IRT; 15-OCT-94.
DR PDB; 1IRP; 27-FEB-95.
DR PDB; 1ILR; 07-FEB-95.
DR PDB; 1ILT; 01-APR-95.
DR PDB; 1IRA; 17-JUN-98.
DR Aarhus/Ghent-2DPAGE; 7104; IEF.
DR Aarhus/Ghent-2DPAGE; 7105; IEF.
DR MIM; 147679; -.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal; Alternative splicing; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.

```
FT   DISULFID     91    141
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     21       MEICRGLRSHLITLLLFLFHS -> MAL (IN
FT                                INTRACELLULAR ISOFORM).
SQ   SEQUENCE   177 AA;  20055 MW;  D1690776A7394057 CRC64;


  Query Match             29.2%;  Score 238.5;  DB 1;  Length 177;
  Best Local Similarity   40.9%;  Pred. No. 5.4e-18;
  Matches   56;  Conservative   18;  Mismatches   56;  Indels    7;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    ||| :|          :|||| ||  ||:||::
Db      44 NQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 98

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :   |||| ||| :| :  ::  || | :| ||     |:|| ||||||   |  ||| |
Db      99 DETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSL 158

Qy     135 TKESEPSAR-TKFYFEQ 150
           |   :     |||||::
       159 TNMPDEGVMVTKFYFQE 175


RESULT   6
IL1X_HORSE
ID   IL1X_HORSE     STANDARD;      PRT;   177 AA.
AC   O18999; O77745;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97366446; PubMed=9223227;
RA   Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,
RA   Tsujimoto H., Hasegawa A.;
RT   "Molecular cloning and functional expression of equine interleukin-1
RT   receptor antagonist.";
RL   Vet. Immunol. Immunopathol. 56:221-231(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98285942; PubMed=9622739;
     Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
     "Cloning of equine interleukin-1 receptor antagonist and
     determination of its full-length cDNA sequence.";
RL   Am. J. Vet. Res. 59:712-716(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D83714; BAA22529.1; -.
DR   EMBL; U92482; AAC39257.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     19     19       F -> L (IN REF. 2).
SQ   SEQUENCE   177 AA;  20459 MW;  1ABC377F1F1CF80B CRC64;


  Query Match             29.1%;  Score 238;  DB 1;  Length 177;
  Best Local Similarity   39.7%;  Pred. No. 6.1e-18;
  Matches   60;  Conservative   19;  Mismatches   62;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           | :   | : :   :||  | |: ||: |     |    |||  :|          :|||
Db      33 CKMQAFRIWDV---NQKTFYMRNNQLVAGYLQESNTKLQEKIDVVPIE-----PDALFLG 84

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           : |   ||||:: :    ||| ||| :| |  ||  |||| :|:||     |:|| |||
Db      85 LHGRKLCLACVKSGDEIRFQLEAVNITDLSKNKEENKRFTFIRSNSGPTTSFESAACPGW 144

Qy     121 FLCGPAEPQQPVQLT-KESEPSARTKFYFEQ 150
           |||   |  :|| || |  |    |||| ::
Db     145 FLCTAQEADRPVSLTNKPKESFMVTKFYLQE 175


RESULT   7
IL1X_BOVIN
ID   IL1X_BOVIN     STANDARD;      PRT;   174 AA.
AC   O77482;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98305607; PubMed=9643454;
RA   Kirisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA   Yoshino T., Iwai H.;
RT   "Enzymatic amplification and expression of bovine interleukin-1
RT   receptor antagonist cDNA.";
RL   Vet. Immunol. Immunopathol. 62:197-208(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB005148; BAA31854.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    174       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     89    139       BY SIMILARITY.
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
SQ   SEQUENCE   174 AA;  19926 MW;  1E56E7F224FF851F CRC64;


  Query Match             28.4%;  Score 232;  DB 1;  Length 174;
  Best Local Similarity   39.1%;  Pred. No. 2.5e-17;
  Matches   59;  Conservative   20;  Mismatches   62;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           |  :   | : :   :||  | |: ||: |     |    |||  :|         :|||
Db      31 CEMQAFRIWDV---NQKIFYLRNNQLVAGYLQGPNTKLEEKIDVVPIE-----PHTMFLG 82

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  |||||:: :   |:|| ||| :| :  |:  || | :  :|     |:|| |||
Db      83 IHGGKLCLACVKSGDEIKLKLEAVNITDLNQNREQDKRFAFIRFDNGPTTSFESAACPGW 142

Qy     121 FLCGPAEPQQPVQLTK-ESEPSARTKFYFEQ 150
           |||   |  ||| ||   :|    |||||:|
Db     143 FLCTSLEADQPVGLTNMPTEALKVTKFYFQQ 173


RESULT   8
IL1B_PIG
ID   IL1B_PIG       STANDARD;      PRT;   267 AA.
AC   P26889;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN   IL1B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93314975; PubMed=8325511;
RA   Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT   "Cloning, sequencing and regulation of an mRNA encoding porcine
RT   interleukin-1 beta.";
RL   Gene 129:285-289(1993).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86725; AAA02584.1; -.
DR   PIR; JN0724; JN0724.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP          1    114       BY SIMILARITY.
FT   CHAIN         115    267       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   267 AA;  30404 MW;  7F6B92B784D5086F CRC64;


  Query Match             16.4%;  Score 134.5;  DB 1;  Length 267;
  Best Local Similarity   31.2%;  Pred. No. 7.3e-07;
  Matches   30;  Conservative   20;  Mismatches   45;  Indels    1;  Gaps    1;

Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: |||:| :  |:||  :  |:||||::  : |   :   || |:::  :    |
Db     169 KIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYKTEIKNRVEFE 227

Qy     114 AAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
           :| :| |::      |:|| |         | |  |
Db     228 SALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263


RESULT   9
IL1B_SHEEP
ID   IL1B_SHEEP     STANDARD;      PRT;   266 AA.
AC   P21621;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN   IL1B.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92119335; PubMed=1840515;
RA   Seow H.F., Rothel J.S., David M.J., Wood P.R.;
RT   "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL   DNA Seq. 1:423-426(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088326; PubMed=2263490;
RA   Fiskerstrand C., Sargan D.;
RT   "Nucleotide sequence of ovine interleukin-1 beta.";
RL   Nucleic Acids Res. 18:7165-7165(1990).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54796; CAA38566.1; -.
DR   EMBL; X56972; CAA40293.1; -.
DR   PIR; S13092; S13092.
```

```
DR   PIR; S13810; S13810.
DR   PIR; S23010; S23010.
DR   HSSP; P01584; 4I1B.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT     14     14       Y -> C (IN REF. 2).
FT   CONFLICT     55     55       Q -> K (IN REF. 2).
FT   CONFLICT     64     64       V -> A (IN REF. 2).
FT   CONFLICT    145    145       P -> L (IN REF. 2).
SQ   SEQUENCE   266 AA;  30717 MW;  BDED07B58224AB78 CRC64;


 Query Match             16.1%;  Score 132;  DB 1;  Length 266;
 Best Local Similarity   25.4%;  Pred. No. 1.3e-06;
 Matches   34;  Conservative   28;  Mismatches   44;  Indels   28;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR--------------TKVPIFLG 60
           :||:|           | |: |  |   ||:: : |                |:|: ||
Db     127 EQKSL------------VLDSPCVLKALHLPSQEMSREVVFCMSFVQGEERDNKIPVALG 174

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           |:  :  |:||:  : |:||||:|:  ::|       || |:::   :    |:  :| |
Db     175 IRDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESVLYPNW 233

Qy     121 FLCGPAEPQQPVQL 134
           ::      ::|| |
Db     234 YISTSQIEEKPVFL 247


RESULT  10
IL1B_MOUSE
ID   IL1B_MOUSE     STANDARD;      PRT;   269 AA.
AC   P10749;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN   IL1B.
OS   Mus musculus (Mouse).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
     NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87058957; PubMed=3491144;
RA   Gray P.W., Glaister D., Chen E., Goeddel D.V., Pennica D.;
RT   "Two interleukin 1 genes in the mouse: cloning and expression of the
RT   cDNA for murine interleukin 1 beta.";
RL   J. Immunol. 137:3644-3648(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87117546; PubMed=3492706;
RA   Telford J.L., Macchia G., Massone A., Carinci V., Palla E., Melli M.;
RT   "The murine interleukin 1 beta gene: structure and evolution.";
RL   Nucleic Acids Res. 14:9955-9963(1986).
RN   [3]
RP   SEQUENCE OF 118-139.
RX   MEDLINE=88229074; PubMed=2967326;
RA   Huang J.J., Newton R.C., Rutledge S.J., Horuk R., Matthew J.B.,
RA   Covington M., Lin Y.;
RT   "Characterization of murine IL-1 beta. Isolation, expression, and
RT   purification.";
RL   J. Immunol. 140:3838-3843(1988).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=92222792; PubMed=1807351;
RA   van Oostrum J., Priestle J.P., Grutter M.G., Schmitz A.;
RT   "The structure of murine interleukin-1 beta at 2.8-A resolution.";
RL   J. Struct. Biol. 107:189-195(1991).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M15131; AAA39276.1; -.
DR   EMBL; X04964; CAA28637.1; -.
DR   PIR; A24719; A24719.
DR   PIR; S13029; S13029.
DR   PDB; 8I1B; 15-OCT-94.
DR   PDB; 2MIB; 31-JAN-94.
DR   MGD; MGI:96543; Il1b.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW   3D-structure.
FT   PROPEP        1    117
FT   CHAIN       118    269       INTERLEUKIN-1 BETA.
FT   STRAND      123    129
FT   TURN        130    131
FT   STRAND      134    137
FT   TURN        140    141
FT   STRAND      143    146
FT   TURN        150    154
FT   STRAND      159    163
FT   TURN        170    171
FT   STRAND      173    179
FT   TURN        180    181
FT   STRAND      184    191
FT   TURN        192    193
FT   STRAND      194    201
FT   TURN        204    206
FT   HELIX       214    216
FT   STRAND      217    222
FT   STRAND      227    231
FT   TURN        235    236
FT   STRAND      238    242
FT   STRAND      247    248
FT   STRAND      250    252
FT   STRAND      258    259
FT   STRAND      262    266
SQ   SEQUENCE   269 AA;  30931 MW;  734FA17B02ED87EE CRC64;
```

```
  Query Match             15.2%;  Score 124.5;  DB 1;  Length 269;
  Best Local Similarity   24.4%;  Pred. No. 8.3e-06;
  Matches   39;  Conservative   28;  Mismatches   52;  Indels   41;  Gaps    5;

Qy       1 MCSLPMAR-YYIIKYADQKALYTRD----------GQ-----------LLVGDPVADNCC 38
           :| :|: : :| ::   ||:|   |          ||           : |:|  |
Db     115 VCDVPIRQLHYRLRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSND--- 171

Qy      39 AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATR 98
                      |:|: ||::| :  |:||  :  |:|||| |: :: |   :   |
Db     172 --------------KIPVALGLKGKNLYLSCVMKDGTPTLQLESVDPKQ-YPKKKMEKR 215

Qy      99 FTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKES 138
           | | :    |    |:| :| |::        :|| |   |
Db     216 FVFNKIEVKSKVEFESAEFPNWYISTSQAEHKPVFLGNNS 255
```

RESULT 11
IL1B_CEREL
ID IL1B_CEREL STANDARD; PRT; 266 AA.
AC P51745;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockhart E.A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
-!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U20500; AAA62234.1; -.
DR HSSP; P01584; 1HIB.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003502; Interleukin_1_prop.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113 BY SIMILARITY.
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
SQ SEQUENCE 266 AA; 30629 MW; 4F40B4E6F0D9F060 CRC64;

```
  Query Match             14.6%;  Score 119.5;  DB 1;  Length 266;
  Best Local Similarity   29.6%;  Pred. No. 2.7e-05;
  Matches   24;  Conservative   22;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: |||:  :: |:||:  : |:||||:|:  ::|       || |:::       |
Db     168 KIPVALGIRDKNQYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKDTVEFE 226

Qy     114 AAAWPGWFLCGPAEPQQPVQL 134
           :  :| |::      ::|| |
Db     227 SVLYPNWYISTSHPEEKPVFL 247
```

RESULT 12
IL1B_BOVIN
ID IL1B_BOVIN STANDARD; PRT; 266 AA.
AC P09428;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89016591; PubMed=3262866;
RA Leong S.R., Flaggs G.M., Lawman M., Gray P.W.;
RT "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";
RL Nucleic Acids Res. 16:9054-9054(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88318652; PubMed=3261832;
RA Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
RA Gillis S., Cerretti D.P.;
RT "Cloning, sequence and expression of bovine interleukin 1 alpha and
RT interleukin 1 beta complementary DNAs.";
RL Mol. Immunol. 25:429-437(1988).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M35589; AAA30585.1; -.
DR EMBL; X12498; CAA31018.1; -.
DR EMBL; M37211; AAA30584.1; -.
DR PIR; JL0010; ICBO1B.
DR PIR; S01380; S01380.

```
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP          1    113
FT   CHAIN         114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT      252    252       A -> G (IN REF. 2).
SQ   SEQUENCE   266 AA;  30774 MW;  9D1EF8F575070586 CRC64;


  Query Match             14.3%;  Score 117;  DB 1;  Length 266;
  Best Local Similarity   29.5%;  Pred. No. 5e-05;
  Matches   26;  Conservative   24;  Mismatches   36;  Indels    2;  Gaps    2;

       48 RGLDR-TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSS 106
          :| :|  |:|: |||:  :  |:||:  : |:||||:|:  ::|       || |:::
      161 QGEERDNKIPVALGIKDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEI 219

Qy    107 GSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
            :   |:  :| |::     ::|| |
Db    220 KNTVEFESVLYPNWYISTSQIEERPVFL 247


RESULT  13
IL1B_RAT
ID   IL1B_RAT       STANDARD;      PRT;   268 AA.
AC   Q63264;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN   IL1B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Macrophage;
RA   Feeser W., Freimark B.D.;
RL   Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M98820; AAA41426.1; -.
DR   HSSP; P10749; 2MIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP          1    116       BY SIMILARITY.
FT   CHAIN         117    268       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   268 AA;  30644 MW;  109C19EBF69C242D CRC64;


  Query Match             13.8%;  Score 112.5;  DB 1;  Length 268;
  Best Local Similarity   23.3%;  Pred. No. 0.00015;
  Matches   35;  Conservative   31;  Mismatches   55;  Indels   29;  Gaps    5;

Qy      1 MCSLPMARYYI-IKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR------- 52
            :| :|: : :  ::   ||        |:: ||     |  |   |  : : :
Db    114 VCDVPIRQLHCRLRDEQQKC-------LVLSDP-----CELKALHLNGQNISQQVVFSMS 161

Qy     53 --------TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQS 104
                  |:|: ||::| :  |:||  :  |:|||| |: :: |   :   || | :
Db    162 FVQGETSNDKIPVALGLKGLNLYLSCVMKDGTPTLQLESVDPKQ-YPKKKMEKRFVFNKI 220

Qy    105 SSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
              :   |:| :| |::      :|| |
Db    221 EVKTKVEFESAQFPNWYISTSQAEHRPVFL 250


RESULT  14
IL1B_CAPHI
ID   IL1B_CAPHI     STANDARD;      PRT;   266 AA.
AC   P79162;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN   IL1B.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT   "Molecular cloning and expression of caprine IL-1alpha and
RT   IL-1beta.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
```

```
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; D63351; BAA09675.1; -.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113       BY SIMILARITY.
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30769 MW;  59F7B39BD1D4DDA5 CRC64;


    ery Match             13.6%;  Score 111;  DB 1;  Length 266;
  Best Local Similarity   23.9%;  Pred. No. 0.00021;
  Matches   32;  Conservative   28;  Mismatches   46;  Indels   28;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR--------------TKVPIFLG 60
           :||:|            | |: |  |   | :: : |                |:|: ||
Db     127 EQKSL-----------VLDSPCVLKALHLLSQEMSREVVFCMSFVQGEERDNKIPVALG 174

Qy      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           |:  :  |: |:  : |:|||:|:  ::|       || |:::   :    |:  :| |
Db     175 IRDKNLYLSWVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESVLYPNW 233

Qy     121 FLCGPAEPQQPVQL 134
           ::      ::|| |
Db     234 YISTSQIEEKPVFL 247


RESULT  15
IL1B_RABIT
ID   IL1B_RABIT     STANDARD;      PRT;   268 AA.
AC   P14628;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (LYMPHOCYTE PROLIFERATION
DE   POTENTIATING FACTOR).
GN   IL1B.
     Oryctolagus cuniculus (Rabbit).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89176242; PubMed=2784458;
RA   Cannon J.G., Clark B.D., Wingfield P., Schmeissner U., Losberger C.,
RA   Dinarello C.A., Shaw A.R.;
RT   "Rabbit IL-1. Cloning, expression, biologic properties, and
RT   transcription during endotoxemia.";
RL   J. Immunol. 142:2299-2306(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88134238; PubMed=2449207;
RA   Mori S., Goto F., Goto K., Ohkawara S., Maeda S., Shimada K.,
RA   Yoshinaga M.;
RT   "Cloning and sequence analysis of a cDNA for lymphocyte proliferation
RT   potentiating factor of rabbit polymorphonuclear leukocytes:
RT   identification rabbit interleukin 1 beta.";
RL   Biochem. Biophys. Res. Commun. 150:1237-1243(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89315718; PubMed=2787507;
RA   Young P.R., Sylvester D.;
RT   "Cloning of rabbit interleukin-1 beta: differential evolution of IL-1
RT   alpha and IL-1 beta proteins.";
RL   Protein Eng. 2:545-551(1989).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; D21835; BAA04863.1; -.
DR   EMBL; M26295; AAA31373.1; -.
DR   PIR; A27714; A27714.
DR   PIR; JU0082; JU0082.
DR   PIR; A30584; A30584.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116
FT   CHAIN       117    268       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   268 AA;  30665 MW;  55BF44DD78D1B297 CRC64;


  Query Match             13.5%;  Score 110.5;  DB 1;  Length 268;
  Best Local Similarity   30.6%;  Pred. No. 0.00024;
  Matches   26;  Conservative   16;  Mismatches   42;  Indels    1;  Gaps    1;

Qy      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
           |:|: ||::| :  |:||  :: |:|||| |:    |   :   || | :        |
Db     170 KIPVALGLRGKNLYLSCVMKDDKPTLQLESVD-PNRYPKKKMEKRFVFNKIEIKDKLEFE 228

Qy     114 AAAWPGWFLCGPAEPQQPVQLTKES 138
           :| :| |::        || |   |
Db     229 SAQFPNWYISTSQTEYMPVFLGNNS 253


Search completed: May 10, 2002, 13:54:03
Job time: 116 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 19, 2002, 04:48:21 ; Search time 82.04 Seconds
(without alignments)
3053.951 Million cell updates/sec

Title: US-09-724-583-1
Perfect score: 1020
Sequence: 1 cagggatcagggttccagga.....acctctaaaaaaaaaaaaaa 1020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	991.2	97.2	998	4	US-09-316-081-1	Sequence 1, Appli
2	991.2	97.2	998	4	US-09-316-081-3	Sequence 3, Appli
3	110.8	10.9	1282	4	US-09-417-455-4	Sequence 4, Appli
4	110.8	10.9	1282	4	US-09-348-942-4	Sequence 4, Appli
5	110.8	10.9	2648	4	US-09-417-455-6	Sequence 6, Appli
6	110.8	10.9	2648	4	US-09-348-942-6	Sequence 6, Appli
7	103.4	10.1	1710	3	US-09-000-630C-1	Sequence 1, Appli
8	103.4	10.1	1710	3	US-08-862-730C-1	Sequence 1, Appli
9	97.4	9.5	176373	3	US-09-128-155-17	Sequence 17, Appl
c 10	97	9.5	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 11	97	9.5	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 12	97	9.5	246240	2	US-08-724-394A-22	Sequence 22, Appl
13	95	9.3	462	3	US-08-798-414-1	Sequence 1, Appli
14	95	9.3	462	4	US-09-131-247-1	Sequence 1, Appli
15	95	9.3	474	1	US-08-476-860-9	Sequence 9, Appli
16	95	9.3	474	2	US-08-910-733-9	Sequence 9, Appli
17	95	9.3	474	2	US-08-910-884-9	Sequence 9, Appli
18	95	9.3	514	1	US-08-284-784-41	Sequence 41, Appl
19	95	9.3	514	2	US-08-854-811-41	Sequence 41, Appl
20	95	9.3	531	2	US-08-809-185-1	Sequence 1, Appli
21	95	9.3	534	3	US-09-000-630C-24	Sequence 24, Appl
22	95	9.3	534	3	US-08-862-730C-24	Sequence 24, Appl
23	95	9.3	543	1	US-08-422-655-1	Sequence 1, Appli
24	95	9.3	579	1	US-08-476-860-12	Sequence 12, Appl
25	95	9.3	579	2	US-08-910-733-12	Sequence 12, Appl
26	95	9.3	579	2	US-08-910-884-12	Sequence 12, Appl
27	95	9.3	602	1	US-08-459-811-1	Sequence 1, Appli
28	95	9.3	602	1	US-08-459-092-1	Sequence 1, Appli
29	95	9.3	602	2	US-08-459-814-1	Sequence 1, Appli
30	95	9.3	602	2	US-08-425-232-1	Sequence 1, Appli
31	95	9.3	602	2	US-08-471-227-2	Sequence 2, Appli
32	95	9.3	603	1	US-08-484-598-1	Sequence 1, Appli
33	95	9.3	603	2	US-08-479-140-1	Sequence 1, Appli
34	95	9.3	603	3	US-08-477-143-1	Sequence 1, Appli
35	95	9.3	717	1	US-08-284-784-40	Sequence 40, Appl
36	95	9.3	717	2	US-08-854-811-40	Sequence 40, Appl
37	94	9.2	537	3	US-09-000-630C-27	Sequence 27, Appl
38	94	9.2	537	3	US-08-862-730C-27	Sequence 27, Appl
39	92.4	9.1	537	3	US-09-000-630C-25	Sequence 25, Appl
40	92.4	9.1	537	3	US-08-862-730C-25	Sequence 25, Appl
41	88.4	8.7	534	3	US-09-000-630C-26	Sequence 26, Appl
42	88.4	8.7	534	3	US-08-862-730C-26	Sequence 26, Appl
43	84.6	8.3	475	4	US-09-131-247-3	Sequence 3, Appli
44	84.6	8.3	1167	4	US-09-131-247-15	Sequence 15, Appl
45	84.6	8.3	1170	4	US-09-131-247-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-316-081-1
; Sequence 1, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(512)
US-09-316-081-1

Query Match 97.2%; Score 991.2; DB 4; Length 998;
Best Local Similarity 99.7%; Pred. No. 9.4e-300;
Matches 993; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      11 ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 60

Qy      71 ccctccccatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ccctccccatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa 120

Qy     131 gagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatct 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatct 180

Qy     191 gcacacttcctaacagaggcttggaccgcaccaaggtccccattttcctggggatccagg 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 gcacacttcctaacagaggcttggaccgcaccaaggtccccattttcctggggatccagg 240

Qy     251 gagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggagg 310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 gagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggagg 300

Qy     311 atgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttcc 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 atgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttcc 360
```

```
Qy    371 agagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgt 430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 agagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgt 420

Qy    431 gtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccctcagccc 490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 gtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccctcagccc 480

Qy    491 gtaccaagttttactttgaacagagctggtagggagacaggaaactgcgttttagccttg 550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gtaccaagttttactttgaacagagctggtagggagacaggaaactgcgttttagccttg 540

Qy    551 tgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccga 610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 tgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccga 600

Qy    611 aatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtccaaagagg 670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 aatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtccaaagagg 660

Qy    671 ttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatcctt 730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatcctt 720

Qy    731 gtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaag 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaag 780

Qy    791 ataccatgcttctaattttgaagatggagtgaggggccttgagccaacaaatgcaggtgt 850
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    781 ataccatgcttctaattttgaagatggagtgaggggccttgagccaacaatgcaggtgt 840

Qy    851 ttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaaggaacac 910
          |||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    841 ttttagaaggaggaaaagccaagggaacggattctcctctatagtctccggaaggaacac 900

Qy    911 agctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctccacaa 970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 agctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctccacaa 960

Qy    971 ctataaaatAATAAACTTGTGTTATTGTAAACCTCT 1006
          |||||||||||||||||||||||||||||||||||
      961 ctataaaatAATAAACTTGTGTTATTGTAAACCTCT 996
```

RESULT 2
US-09-316-081-3
; Sequence 3, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(512)
US-09-316-081-3

Query Match 97.2%; Score 991.2; DB 4; Length 998;
Best Local Similarity 99.7%; Pred. No. 9.4e-300;
Matches 993; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy     11 ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 70
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 60

Qy     71 ccctccccatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ccctccccatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa 120

Qy    131 gagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatct 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatct 180

Qy    191 gcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctggggatccagg 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 gcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctggggatccagg 240

Qy    251 gagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggagg 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 gagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggagg 300

Qy    311 atgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttcc 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 atgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttcc 360

Qy    371 agagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgt 430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 agagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgt 420

Qy    431 gtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccctcagccc 490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 gtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccctcagccc 480

Qy    491 gtaccaagttttactttgaacagagctggtagggagacaggaaactgcgttttagccttg 550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gtaccaagttttactttgaacagagctggtagggagacaggaaactgcgttttagccttg 540

Qy    551 tgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccga 610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 tgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccga 600

Qy    611 aatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtccaaagagg 670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 aatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtccaaagagg 660

Qy    671 ttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatcctt 730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatcctt 720

Qy    731 gtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaag 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaag 780

Qy    791 ataccatgcttctaattttgaagatggagtgaggggccttgagccaacaaatgcaggtgt 850
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    781 ataccatgcttctaattttgaagatggagtgaggggccttgagccaacatatgcaggtgt 840

Qy    851 ttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaaggaacac 910
          |||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    841 ttttagaaggaggaaaagccaagggaacggattctcctctatagtctccggaaggaacac 900

Qy    911 agctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctccacaa 970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 agctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctccacaa 960

Qy    971 ctataaaatAATAAACTTGTGTTATTGTAAACCTCT 1006
          |||||||||||||||||||||||||||||||||||
Db    961 ctataaaatAATAAACTTGTGTTATTGTAAACCTCT 996
```

RESULT 3
US-09-417-455-4
; Sequence 4, Application US/09417455
; Patent No. 6294655

```
; GENERAL INFORMATION:
;  APPLICANT: Ford, John
;  APPLICANT:  Pace, Ann
;  TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
;  FILE REFERENCE: 28110/36328
;  CURRENT APPLICATION NUMBER: US/09/417,455
;  CURRENT FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER: US 09/348,942
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: PCT/US99/04291
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: US 09/287,210
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: US 09/251,370
;  PRIOR FILING DATE: 1999-02-17
;  PRIOR APPLICATION NUMBER: US 09/229,591
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 09/127,698
;  PRIOR FILING DATE: 1998-07-31
;  PRIOR APPLICATION NUMBER: US 09/099,818
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: US 09/082,364
;  PRIOR FILING DATE: 1998-05-20
;  PRIOR APPLICATION NUMBER: US 09/079,909
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 09/055,010
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 1282
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (73)...(537)
US-09-417-455-4


  Query Match           10.9%;  Score 110.8;  DB 4;  Length 1282;
  Best Local Similarity  58.6%;  Pred. No. 1e-24;
  Matches  231;  Conservative    0;  Mismatches  157;  Indels    6;  Gaps    2;

Qy      81 ggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcca 140
           |||    | || |  ||| ||  |  | |    |||||  || ||         ||  |||
Db      87 ggcgctgtgcttccgaatgaaggactcggcattgaaggtgctttatctgcataataacca 146

Qy     141 gctgctggtgggagatcctgttgcagacaactgctgt---gcagagaagatctgcacact 197
           ||| || |  ||||  |    |||||  ||   |  |   |  ||  |||||  ||    |
Db     147 gcttctagctggagggctgcatgcagggaaggtcattaaaggtgaagagatcagcgtggt 206

Qy     198 tcctaacagaggcttggaccgcaccaaggtccccatttcctggggatccagggagggag 257
           || ||  |  | ||||   || |  |  |||| |  |||||||  ||||||| || ||
Db     207 ccccaatcggtggctggatgccagcctgtcccccgtcatcctgggtgtccagggtggaag 266

Qy     258 ccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggaggatgtgaa 317
           ||  |||||| |||||| || |    |   ||| |||  | |||   || |||   |||||
Db     267 ccagtgcctgtcatgtggggtg---gggcaggagccgactctaacactagagccagtgaa 323

Qy     318 cattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcag 377
           |||   ||| || ||    ||||   | ||  |||   ||||||||||||| || | |
Db     324 catcatggagctctatcttggtgccaaggaatccaagagcttcaccttctaccggcggga 383

Qy     378 ctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgtgtggccc 437
           |   ||   | ||| |||  | ||| | |||||||  || ||||||||||||||
Db     384 catggggctcacctccagcttcgagtcggctgcctacccgggctggttcctgtgcacggt 443

Qy     438 ggcagagccccagcagccagtacagctcaccaag 471
           | | ||  || | ||||| ||    |||||| ||
Db     444 gcctgaagccgatcagcctgtcagactcacccag 477


RESULT   4
```

```
US-09-348-942-4
; Sequence 4, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
;  APPLICANT: John Ford
;  TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
;  FILE REFERENCE: 28110/35801
;  CURRENT APPLICATION NUMBER: US/09/348,942
;  CURRENT FILING DATE: 1999-07-07
;  EARLIER APPLICATION NUMBER: PCT/US99/04291
;  EARLIER FILING DATE: 1999-04-05
;  EARLIER APPLICATION NUMBER: US 09/287,210
;  EARLIER FILING DATE: 1999-04-05
;  EARLIER APPLICATION NUMBER: US 09/251,370
;  EARLIER FILING DATE: 1999-02-17
;  EARLIER APPLICATION NUMBER: US 09/229,591
;  EARLIER FILING DATE: 1999-01-13
;  EARLIER APPLICATION NUMBER: US 09/127,698
;  EARLIER FILING DATE: 1998-07-31
;  EARLIER APPLICATION NUMBER: US 09/099,818
;  EARLIER FILING DATE: 1998-06-19
;  EARLIER APPLICATION NUMBER: US 09/082,364
;  EARLIER FILING DATE: 1998-05-20
;  EARLIER APPLICATION NUMBER: US 09/079,909
;  EARLIER FILING DATE: 1998-05-15
;  EARLIER APPLICATION NUMBER: US 09/055,010
;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 1282
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (73)...(537)
US-09-348-942-4


  Query Match           10.9%;  Score 110.8;  DB 4;  Length 1282;
  Best Local Similarity  58.6%;  Pred. No. 1e-24;
  Matches  231;  Conservative    0;  Mismatches  157;  Indels    6;  Gaps    2;

Qy      81 ggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcca 140
           |||    | || |  ||| ||  |  | |    |||||  || ||         ||  |||
Db      87 ggcgctgtgcttccgaatgaaggactcggcattgaaggtgctttatctgcataataacca 146

Qy     141 gctgctggtgggagatcctgttgcagacaactgctgt---gcagagaagatctgcacact 197
           ||| || |  ||||  |    |||||  ||   |  |   |  ||  |||||  ||    |
Db     147 gcttctagctggagggctgcatgcagggaaggtcattaaaggtgaagagatcagcgtggt 206

Qy     198 tcctaacagaggcttggaccgcaccaaggtccccatttcctggggatccagggagggag 257
           || ||  |  | ||||   || |  |  |||| |  |||||||  ||||||| || ||
Db     207 ccccaatcggtggctggatgccagcctgtcccccgtcatcctgggtgtccagggtggaag 266

Qy     258 ccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggaggatgtgaa 317
           ||  |||||| |||||| || |    |   ||| |||  | |||   || |||   |||||
Db     267 ccagtgcctgtcatgtggggtg---gggcaggagccgactctaacactagagccagtgaa 323

Qy     318 cattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcag 377
           |||   ||| || ||    ||||   | ||  |||   ||||||||||||| || | |
Db     324 catcatggagctctatcttggtgccaaggaatccaagagcttcaccttctaccggcggga 383

Qy     378 ctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgtgtggccc 437
           |   ||   | ||| |||  | ||| | |||||||  || ||||||||||||||
Db     384 catggggctcacctccagcttcgagtcggctgcctacccgggctggttcctgtgcacggt 443

Qy     438 ggcagagccccagcagccagtacagctcaccaag 471
           | | ||  || | ||||| ||    |||||| ||
Db     444 gcctgaagccgatcagcctgtcagactcacccag 477


RESULT   5
```

US-09-417-455-6
; Sequence 6, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-417-455-6

Query Match 10.9%; Score 110.8; DB 4; Length 2648;
Best Local Similarity 58.6%; Pred. No. 1.6e-24;
Matches 231; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

```
Qy      81 ggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcca 140
           |||    | || |  ||| ||  |  | |    |||||  || ||        ||  |||
Db      76 ggcgctgtgcttccgaatgaaggactcggcattgaaggtgctttatctgcataataacca 135

Qy     141 gctgctggtgggagatcctgttgcagacaactgctgt---gcagagaagatctgcacact 197
           ||| || |  ||||  |    |||||  ||   |  |   |  ||  ||||| ||    |
Db     136 gcttctagctggagggctgcatgcagggaaggtcattaaaggtgaagagatcagcgtggt 195

Qy     198 tcctaacagaggcttggaccgcaccaaggtccccatttttcctggggatccagggagggag 257
           || ||  |  |  ||||   || |  |  |||| |  |||||||  ||||||| || ||
Db     196 ccccaatcggtggctggatgccagcctgtcccccgtcatcctgggtgtccagggtggaag 255

Qy     258 ccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggaggatgtgaa 317
           ||  ||||||| |||||| || |   |   ||| |||  | |||   || |||   |||||
Db     256 ccagtgcctgtcatgtggggtg---gggcaggagccgactctaacactagagccagtgaa 312

Qy     318 cattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcag 377
           |||   ||| || ||    ||||   | ||  |||   ||||||||||| || | |
Db     313 catcatggagctctatcttggtgccaaggaatccaagagcttcaccttctaccggcggga 372

Qy     378 ctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgtgtggccc 437
           |   ||   | ||| |||  | ||| | |||||||  || ||||||||||||||
Db     373 catggggctcacctccagcttcgagtcggctgcctacccgggctggttcctgtgcacggt 432

Qy     438 ggcagagccccagcagccagtacagctcaccaag 471
           | | ||  || | ||||| ||    |||||| ||
Db     433 gcctgaagccgatcagcctgtcagactcacccag 466
```

RESULT 6

US-09-348-942-6
; Sequence 6, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-348-942-6

Query Match 10.9%; Score 110.8; DB 4; Length 2648;
Best Local Similarity 58.6%; Pred. No. 1.6e-24;
Matches 231; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

```
Qy      81 ggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcca 140
           |||    | || |  ||| ||  |  | |    |||||  || ||        ||  |||
Db      76 ggcgctgtgcttccgaatgaaggactcggcattgaaggtgctttatctgcataataacca 135

Qy     141 gctgctggtgggagatcctgttgcagacaactgctgt---gcagagaagatctgcacact 197
           ||| || |  ||||  |    |||||  ||   |  |   |  ||  ||||| ||    |
Db     136 gcttctagctggagggctgcatgcagggaaggtcattaaaggtgaagagatcagcgtggt 195

Qy     198 tcctaacagaggcttggaccgcaccaaggtccccatttttcctggggatccagggagggag 257
           || ||  |  |  ||||   || |  |  |||| |  |||||||  ||||||| || ||
Db     196 ccccaatcggtggctggatgccagcctgtcccccgtcatcctgggtgtccagggtggaag 255

Qy     258 ccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggaggatgtgaa 317
           ||  ||||||| |||||| || |   |   ||| |||  | |||   || |||   |||||
Db     256 ccagtgcctgtcatgtggggtg---gggcaggagccgactctaacactagagccagtgaa 312

Qy     318 cattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcag 377
           |||   ||| || ||    ||||   | ||  |||   ||||||||||| || | |
Db     313 catcatggagctctatcttggtgccaaggaatccaagagcttcaccttctaccggcggga 372

Qy     378 ctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgtgtggccc 437
           |   ||   | ||| |||  | ||| | |||||||  || ||||||||||||||
Db     373 catggggctcacctccagcttcgagtcggctgcctacccgggctggttcctgtgcacggt 432

Qy     438 ggcagagccccagcagccagtacagctcaccaag 471
           | | ||  || | ||||| ||    |||||| ||
Db     433 gcctgaagccgatcagcctgtcagactcacccag 466
```

RESULT 7
US-09-000-630C-1
; Sequence 1, Application US/09000630C
; Patent No. 6018029

```
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,630C
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/862,730
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1710 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;      CELL TYPE:  canine peripheral blood macrophage
;      CELL LINE:  primary monocytes
;    IMMEDIATE SOURCE:
;      LIBRARY:  lambda gt11 cDNA
;      CLONE:  Canine IL-1ra
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1 to 1710
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  open reading frame
;      LOCATION:  60 to 587
;      OTHER INFORMATION:
US-09-000-630C-1


  Query Match             10.1%;  Score 103.4;  DB 3;  Length 1710;
   est Local Similarity   64.3%;  Pred. No. 2.5e-22;
   atches  155;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy    230 ccattttcctggggatccagggagggagccgctgcctggcatgtgtggagacagaagagg 289
          || | ||| |||||||||| || ||||  |  |||||||| |||||  || | | ||| |
Db    298 CCGTGTTCTTGGGGATCCATGGGGGGAAGCTGTGCCTGGCCTGTGTCAAGTCTGGAGATG 357

Qy    290 ggccttccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagagg 349
           | |    || ||||||||||  || |||||    || |||   ||       ||  | |
Db    358 AGACCAGGCTCCAGCTGGAGGCCGTTAACATCACTGACCTGAGTAAGAACAAGGATCAAG 417

Qy    350 ccacacgcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctg 409
           ||  ||||| |||||| |||       |   ||| || ||  |||  ||||| ||||||
Db    418 ACAAGCGCTTTACCTTCATCCTCTCAGACAGTGGCCCCACCACCAGCTTTGAGTCTGCTG 477

Qy    410 cctggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcacca 469
          |||| ||||||||||||||| ||      |    ||| || | | ||| ||    |||||||
Db    478 CCTGCCCTGGCTGGTTCCTCTGCACAGCACTGGAGGCCGACCGGCCTGTCAGCCTCACCA 537

Qy    470 a 470
          |
Db    538 A 538


RESULT   8
US-08-862-730C-1
; Sequence 1, Application US/08862730C
; Patent No. 6063600
;  GENERAL INFORMATION:
;    APPLICANT:  Fuller, Gerald M
;    APPLICANT:  Fuentes, Nelson L.
;    TITLE OF INVENTION:  DNA Encoding Canine Interleukin-1 Receptor
;    TITLE OF INVENTION:  Antagonist
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Douglas C Murdock/ Bradley, Arant, Rose & White
;      STREET:  2001 Park Place, Suite 1400
;      CITY:  Birmingham
;      STATE:  Alabama
;      COUNTRY:  USA
;      ZIP:  35203-2736
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Microsoft Windows
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,730C
;      FILING DATE:  5/23/97
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1710 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;      CELL TYPE:  canine peripheral blood macrophage
;      CELL LINE:  primary monocytes
;    IMMEDIATE SOURCE:
;      LIBRARY:  lambda gt11 cDNA
;      CLONE:  Canine IL-1ra
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1 to 1710
;      OTHER INFORMATION:
;    FEATURE:
;      NAME/KEY:  open reading frame
;      LOCATION:  60 to 587
;      OTHER INFORMATION:
US-08-862-730C-1


  Query Match             10.1%;  Score 103.4;  DB 3;  Length 1710;
  Best Local Similarity   64.3%;  Pred. No. 2.5e-22;
  Matches  155;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy    230 ccattttcctggggatccagggagggagccgctgcctggcatgtgtggagacagaagagg 289
          || | ||| |||||||||| || ||||  |  |||||||| |||||  || | | ||| |
Db    298 CCGTGTTCTTGGGGATCCATGGGGGGAAGCTGTGCCTGGCCTGTGTCAAGTCTGGAGATG 357

Qy    290 ggccttccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagagg 349
           | |    || ||||||||||  || |||||    || |||   ||       ||  | |
Db    358 AGACCAGGCTCCAGCTGGAGGCCGTTAACATCACTGACCTGAGTAAGAACAAGGATCAAG 417

Qy    350 ccacacgcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctg 409
           ||  ||||| |||||| |||       |   ||| || ||  |||  ||||| ||||||
Db    418 ACAAGCGCTTTACCTTCATCCTCTCAGACAGTGGCCCCACCACCAGCTTTGAGTCTGCTG 477

Qy    410 cctggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcacca 469
          |||| ||||||||||||||| ||      |    ||| || | | ||| ||    |||||||
```

```
Db    478 CCTGCCCTGGCTGGTTCCTCTGCACAGCACTGGAGGCCGACCGGCCTGTCAGCCTCACCA 537

Qy    470 a 470
          |
Db    538 A 538


RESULT   9
US-09-128-155-17/c
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 176373
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(176373)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17


  Query Match             9.5%;  Score 97.4;  DB 3;  Length 176373;
  Best Local Similarity   62.1%;  Pred. No. 2.9e-19;
  Matches  259;  Conservative    0;  Mismatches  141;  Indels   17;  Gaps    6;

Qy    585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagat-ctgtgc 643
          ||| |||||||||||||| | |||  || ||||||||||| |||||||| |||  |||||
Db 160498 ATGATAGGCAGAATAATGGCACCCCGAAAATGTCCACATTCTAATCCCCAGACCCTGTGT 160439

Qy    644 atatgttaccatacatgtccaaagaggttttgcaaatgtgatt-atgttaaggatcttga 702
          |||||||||   ||||  | |||| |  ||||||  ||||||| | ||||||  ||||
Db 160438 ATATGTTACATGACATAGCAAAAGGGACTTTGCATCTGTGATTAAAGTTAAGCCTCTTTG 160379

Qy    703 aatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag---------a 753
          |    |||||  |||||||  |  |       | |  |  | |||  ||||         |
Db 160378 AGACGGGAGAGTATCCTGGATATTGACGTGAGCCCGATGTAAATTGCAAGCGTTCTTATA 160319

Qy    754 aggaggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaag 813
          |       | | ||    |   | |||| |  | ||          |  |    |
Db 160318 TGTGAAAGAGGAAGGCAGGAGGGTCAGAGCAAAGCAGTGTGAGAAAAACCCAAGCAGCGA 160259

Qy    814 atggagtgaggggccttgagccaacaaatgcaggt-gtttttagaaggtggaaaagccaa 872
          |   |    |||||  ||||||  |||||||||  |  | | |||| ||||||||  |||
Db 160258 AGATGGGAGTGGGCCACTAGCCAAGGAATGCAGGTGGCCTCTGGAAGCTGGAAAAGGCAA 160199

Qy    873 gggaacggattctcctctagagtctccggaaggaa--cacagctcttgacacatggattt 930
          || ||  || |||||  |||||| ||||  ||| ||  |    ||  ||| || | |||||
Db 160198 GGAAATTGACTCTCCCCTAGAGCCTCCCAAAGCAATGCTATCCTGCTGATACTTTGATTT 160139

Qy    931 cagctcagtgacacccatttcagacttctgacctccacaactataaaataataaact 987
            || |||||| || |||| ||||   |||||||||| ||||  || ||||||  | |
Db 160138 TGGCCCAGTGAGACACATTCCAGA---CTGACCTCCATAACTGCAAGATAATACATT 160085


RESULT  10
US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;     APPLICANT:  Feder, John N.
;     APPLICANT:  Kronmal, Gregory S.
;     APPLICANT:  Lauer, Peter M.
;     APPLICANT:  Ruddy, David A.
;     APPLICANT:  Thomas, Winston
;     APPLICANT:  Tsuchihashi, Zenta
;     APPLICANT:  Wolff, Roger K.
;     TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;     TITLE OF INVENTION:  Sequences and Antibodies Thereto
;     NUMBER OF SEQUENCES:  31
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;       STREET:  Two Embarcadero Center, 8th Floor
;       CITY:  San Francisco
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/724,394A
;       FILING DATE:  01-OCT-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fitts, Renee A.
;       REGISTRATION NUMBER:  35,136
;       REFERENCE/DOCKET NUMBER:  017957-000100
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-576-0200
;       TELEFAX:  415-576-0300
;   INFORMATION FOR SEQ ID NO:  20:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  246240 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1..246240
;       OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-20


  Query Match             9.5%;  Score 97;  DB 2;  Length 246240;
  Best Local Similarity   62.1%;  Pred. No. 4.7e-19;
  Matches  259;  Conservative    0;  Mismatches  140;  Indels   18;  Gaps    6;

Qy    585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgca 644
          | ||||||| ||||  ||||| || ||       |     |  |  ||||  | ||||  |
Db  37190 AGGGTAGGCTGAATGTTGTCCTCCAAAGATATCCATGTCCTAATCCCCAGAACCTGTAAA 37131

Qy    645 tatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaa 704
          ||| ||||| || ||| | |||| |  ||| ||  | | || | ||||||  || |||| |
Db  37130 TATATTACCTTATATGACAAAAGGGACTTTACATGTTTAATAA-GTTAAGAATTTTGAGA 37072

Qy    705 tgaggagacaatcctgggttatccttgtgggctc-agtttaatcacaag-------aagg 756
          || | |||   |||||  || | |   ||||| | ||| ||||||||||         |
Db  37071 TGGGCAGATTTTCCTGAATTTTGCAGATGGGCCCTAGTGTAATCACAAGGGTCCTTATAA 37012

Qy    757 aggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatg 816
            |   | | |||||||||   |||    || |   || | |  ||   |    | |
Db  37011 GAGACAGGCAGAAGAGTCAGAATAAGAGAAAAATACTTCAAGATGTTACACTGCTGGCTT 36952

Qy    817 gagtgagg------ggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagcc 870
            | | ||      ||||  ||||||| ||||||||  ||   || ||| | ||||||
Db  36951 TAAGGTGGAGGAAAGGCCAAGAGCCAAAAAATGCAGTGGTCACTACAAGCT-GAAAAGAA 36893

Qy    871 aagggaacggattctcctctagagtctccggaaggaacacagc--tcttgacacatggat 928
          || | || ||||| ||| ||| || ||| ||| ||  |||| |  |    | || | |||
```

```
Db  36892 AAAGAAATGGATTTTCCCCTAAAGCCTCTGGAGGGGGCACAACCTTGCCAATACCTTGAT 36833

Qy    929 ttcagctcagtgacacccatttcagacttctgacctccacaactataaaataataaa 985
          ||  |||||||||| |||||||| ||||||||||||  | || | ||||  ||||||
Db  36832 TTTGGCTCAGTGAAACCCATTTTGGACTTCTGACCTTTAGAATTGTAAATAAATAAA 36776


RESULT  11
US-08-724-394A-21/c
; Sequence 21, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
     FEATURE:
       NAME/KEY:  misc_feature
       LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-21


  Query Match             9.5%;  Score 97;  DB 2;  Length 246240;
  Best Local Similarity   62.1%;  Pred. No. 4.7e-19;
  Matches  259;  Conservative    0;  Mismatches  140;  Indels   18;  Gaps    6;

Qy    585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgca 644
          | ||||||| ||||  ||||| || ||      |     |  |  ||||  | ||||  |
Db  37190 AGGGTAGGCTGAATGTTGTCCTCCAAAGATATCCATGTCCTAATCCCCAGAACCTGTAAA 37131

Qy    645 tatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaa 704
          ||| ||||| || ||| | |||| |  ||| ||  | | || | |||||| || |||| |
Db  37130 TATATTACCTTATATGACAAAAGGGACTTTACATGTTTAATAA-GTTAAGAATTTTGAGA 37072

Qy    705 tgaggagacaatcctgggttatccttgtgggctc-agtttaatcacaag-------aagg 756
          || | |||   |||||  || | |   ||||| | ||| ||||||||||       |
Db  37071 TGGGCAGATTTTCCTGAATTTTGCAGATGGGCCCTAGTGTAATCACAAGGGTCCTTATAA 37012

Qy    757 aggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatg 816
          |   |   | |||||||||   |||    || |   || | |  ||   |    | |
Db  37011 GAGACAGGCAGAAGAGTCAGAATAAGAGAAAAATACTTCAAGATGTTACACTGCTGGCTT 36952

Qy    817 gagtgagg------ggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagcc 870
          |  | ||      ||||  ||||||| |||||||  ||   || ||| | ||||||
Db  36951 TAAGGTGGAGGAAAGGCCAAGAGCCAAAAAATGCAGTGGTCACTACAAGCT-GAAAAGAA 36893

Qy    871 aagggaacggattctcctctagagtctccggaaggaacacagc--tcttgacacatggat 928
          || | || ||||| ||| ||| || ||| ||| ||  |||| |  |    | || | |||
Db  36892 AAAGAAATGGATTTTCCCCTAAAGCCTCTGGAGGGGGCACAACCTTGCCAATACCTTGAT 36833

Qy    929 ttcagctcagtgacacccatttcagacttctgacctccacaactataaaataataaa 985
          ||  |||||||||| |||||||| ||||||||||||  | || | ||||  ||||||
Db  36832 TTTGGCTCAGTGAAACCCATTTTGGACTTCTGACCTTTAGAATTGTAAATAAATAAA 36776


RESULT  12
US-08-724-394A-22/c
; Sequence 22, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-22


  Query Match             9.5%;  Score 97;  DB 2;  Length 246240;
  Best Local Similarity   62.1%;  Pred. No. 4.7e-19;
```

```
  Matches  259;  Conservative    0;  Mismatches  140;  Indels   18;  Gaps    6;

Qy     585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgca 644
           | ||||||| ||||  ||||| || ||      |     |  |  ||||  | ||||  |
Db   37190 AGGGTAGGCTGAATGTTGTCCTCCAAAGATATCCATGTCCTAATCCCCAGAACCTGTAAA 37131

Qy     645 tatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaa 704
           ||| ||||| || ||| | |||| |  ||| ||  | | || | |||||| || |||| |
Db   37130 TATATTACCTTATATGACAAAAGGGACTTTACATGTTTAATAA-GTTAAGAATTTTGAGA 37072

Qy     705 tgaggagacaatcctgggttatccttgtgggctc-agtttaatcacaag-------aagg 756
           || | |||   |||||  || | |   ||||| | ||| ||||||||||       |
Db   37071 TGGGCAGATTTTCCTGAATTTTGCAGATGGGCCCTAGTGTAATCACAAGGGTCCTTATAA 37012

Qy     757 aggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatg 816
             |   |   | |||||||||   |||    || |   || | |  ||   |    | |
Db   37011 GAGACAGGCAGAAGAGTCAGAATAAGAGAAAAATACTTCAAGATGTTACACTGCTGGCTT 36952

Qy     817 gagtgagg------ggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagcc 870
             | | ||      ||||  ||||||| |||||||| ||   || ||| | ||||||
Db   36951 TAAGGTGGAGGAAAGGCCAAGAGCCAAAAAATGCAGTGGTCACTACAAGCT-GAAAAGAA 36893

Qy     871 aagggaacggattctcctctagagtctccggaaggaacacagc--tcttgacacatggat 928
           || | || ||||| ||| ||| || ||| ||| ||  |||| |  |    | || | |||
Db   36892 AAAGAAATGGATTTTCCCCTAAAGCCTCTGGAGGGGGCACAACCTTGCCAATACCTTGAT 36833

Qy     929 ttcagctcagtgacacccatttcagacttctgacctccacaactataaaataataaa 985
           ||  |||||||||| ||||||||  ||||||||||||  | || | ||||  ||||||
Db   36832 TTTGGCTCAGTGAAACCCATTTTGGACTTCTGACCTTTAGAATTGTAAATAAATAAA 36776


RESULT  13
US-08-798-414-1
; Sequence 1, Application US/08798414
; Patent No. 6096728
;  GENERAL INFORMATION:
;    APPLICANT:  COLLINS, David S.
;    APPLICANT:  BEVILACQUA, Michael P.
;    TITLE OF INVENTION:  COMPOSITION AND METHOD FOR TREATING
;    TITLE OF INVENTION:  INFLAMMATORY DISEASES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
       STREET:  1840 De Havilland Drive
       CITY:  Thousand Oaks
       STATE:  California
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,414
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,419
;      FILING DATE:  09-FEB-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,789
;      FILING DATE:  06-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US (Atty Dkt# A-365B-P)
;      FILING DATE:  23-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ZINDRICK, Thomas D.
;      REGISTRATION NUMBER:  32,185
;      REFERENCE/DOCKET NUMBER:  A-365C
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..462
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..3
;      OTHER INFORMATION:  /note= "Initial methionine is
;      OTHER INFORMATION:  optional."
US-08-798-414-1


  Query Match             9.3%;  Score 95;  DB 3;  Length 462;
  Best Local Similarity   61.5%;  Pred. No. 4.8e-20;
  Matches  152;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy     233 ttttcctggggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggc 292
           | ||| |||| ||||| |||||||     |||||| | |||||  || | |  || | |
Db     170 TGTTCTTGGGAATCCATGGAGGGAAGATGTGCCTGTCCTGTGTCAAGTCTGGTGATGAGA 229

Qy     293 cttccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggcca 352
           |    || ||||||||||  || |||||    || |||  | |      |  |  ||| ||
Db     230 CCAGACTCCAGCTGGAGGCAGTTAACATCACTGACCTGAGCGAGAACAGAAAGCAGGACA 289

Qy     353 cacgcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcct 412
             |||||| ||||| |||        |   ||| || ||  |||  ||||| |||| ||||
Db     290 AGCGCTTCGCCTTCATCCGCTCAGACAGTGGCCCCACCACCAGTTTTGAGTCTGCCGCCT 349

Qy     413 ggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaagg 472
           | || || |||||||| ||      ||   ||  |  | ||||| ||    ||||||||
Db     350 GCCCCGGTTGGTTCCTCTGCACAGCGATGGAAGCTGACCAGCCCGTCAGCCTCACCAATA 409

Qy     473 agagtga 479
             |  |||
Db     410 TGCCTGA 416


RESULT  14
US-09-131-247-1
; Sequence 1, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C.
;  APPLICANT: Hershenson, Susan
;  APPLICANT: Bevilacqua, Michael P.
;  APPLICANT: Collins, David S.
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
;  TITLE OF INVENTION: DISEASES
;  FILE REFERENCE: A-365F
;  CURRENT APPLICATION NUMBER: US/09/131,247
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 60/055,185
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: PCT/US 97/02131
;  EARLIER FILING DATE: 1997-02-10
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(462)
;   OTHER INFORMATION: Initial methionine is optional
US-09-131-247-1


  Query Match             9.3%;  Score 95;  DB 4;  Length 462;
  Best Local Similarity   61.5%;  Pred. No. 4.8e-20;
```

```
  Matches  152;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy     233 ttttcctggggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggc 292
           | ||| |||| ||||| ||||||| |||||| | ||||| || | |  || | |
Db     170 tgttcttgggaatccatggagggaagatgtgcctgtcctgtgtcaagtctggtgatgaga 229

Qy     293 cttccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggcca 352
           |    || ||||||||||  || |||||    || |||  | |     |  |  ||| ||
Db     230 ccagactccagctggaggcagttaacatcactgacctgagcgagaacagaaagcaggaca 289

Qy     353 cacgcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcct 412
             |||||| ||||| |||       |   ||| || ||  |||  ||||| |||| ||||
Db     290 agcgcttcgccttcatccgctcagacagtggccccaccaccagttttgagtctgccgcct 349

Qy     413 ggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaagg 472
           | || || |||||||| ||     ||   ||  |  | ||||| ||    ||||||||
Db     350 gccccggttggttcctctgcacagcgatggaagctgaccagcccgtcagcctcaccaata 409

Qy     473 agagtga 479
             |  |||
Db     410 tgcctga 416


RESULT  15
-08-476-860-9
; Sequence 9, Application US/08476860
; Patent No. 5739282
;  GENERAL INFORMATION:
;    APPLICANT:  COLOTTA, Francesco
;    APPLICANT:  MUZIO, Marta
;    APPLICANT:  MANTOVANI, Alberto
;    TITLE OF INVENTION:  IL-1 ANTAGONIST
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,860
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IT MI 94 A 002097
;      FILING DATE:  13-OCT-1994
     ATTORNEY/AGENT INFORMATION:
       NAME:  BROWDY, Roger L.
       REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  COLOTTA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      OTHER INFORMATION:  Common IL-1ra sequence; a nucleotide G
;      OTHER INFORMATION:  was added in the first position, for computer program
;      OTHER INFORMATION:  reason,  in order to encode the first amino acid  Glu
;      OTHER INFORMATION:  and further in order to avoid the creation of a  stop
;      OTHER INFORMATION:  codon in the inner region of the sequence
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..468
US-08-476-860-9


  Query Match             9.3%;  Score 95;  DB 1;  Length 474;
  Best Local Similarity   61.5%;  Pred. No. 4.9e-20;
  Matches  152;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy     233 ttttcctggggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggc 292
           | ||| |||| ||||| ||||||| |||||| | ||||| || | |  || | |
Db     179 TGTTCTTGGGAATCCATGGAGGGAAGATGTGCCTGTCCTGTGTCAAGTCTGGTGATGAGA 238

Qy     293 cttccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggcca 352
           |    || ||||||||||  || |||||    || |||  | |     |  |  ||| ||
Db     239 CCAGACTCCAGCTGGAGGCAGTTAACATCACTGACCTGAGCGAGAACAGAAAGCAGGACA 298

Qy     353 cacgcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcct 412
             |||||| ||||| |||       |   ||| || ||  |||  ||||| |||| ||||
Db     299 AGCGCTTCGCCTTCATCCGCTCAGACAGTGGCCCCACCACCAGTTTTGAGTCTGCCGCCT 358

Qy     413 ggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaagg 472
           | || || |||||||| ||     ||   ||  |  | ||||| ||    ||||||||
Db     359 GCCCCGGTTGGTTCCTCTGCACAGCGATGGAAGCTGACCAGCCCGTCAGCCTCACCAATA 418

Qy     473 agagtga 479
             |  |||
Db     419 TGCCTGA 425


Search completed: May 19, 2002, 08:49:59
Job time: 14498 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 10, 2002, 13:51:47 ; Search time 24.69 Seconds
(without alignments)
900.502 Million cell updates/sec

Title: US-09-724-583-2
Perfect score: 818
Sequence: 1 MCSLPMARYYIIKYADQKAL.....QLTKESEPSARTKFYFEQSW 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	592	72.4	144	4	Q9BYX1	Q9byx1 homo sapien
2	309	37.8	156	11	Q9JIG2	Q9jig2 mus musculu
3	307	37.5	155	11	Q9QYY1	Q9qyy1 mus musculu
4	283	34.6	155	4	Q9UBH0	Q9ubh0 homo sapien
5	257.5	31.5	159	11	O70207	O70207 mus musculu
6	248	30.3	176	6	Q9BEH0	Q9beh0 canis famil
7	245	30.0	177	6	Q9GMZ4	Q9gmz4 tursiops tr
8	238.5	29.2	143	4	Q9UPC0	Q9upc0 homo sapien
9	238.5	29.2	180	4	Q14628	Q14628 homo sapien
10	238	29.1	176	6	Q9GKK2	Q9gkk2 canis famil
11	177.5	21.7	169	4	Q9NZH8	Q9nzh8 homo sapien
12	176	21.5	157	4	Q9UHA5	Q9uha5 homo sapien
13	172	21.0	183	11	Q9D6Z6	Q9d6z6 mus musculu
14	169	20.7	158	4	Q9UHA7	Q9uha7 homo sapien
15	164.5	20.1	72	6	O77771	O77771 equus cabal
16	156	19.1	178	4	Q9HBF2	Q9hbf2 homo sapien
17	155.5	19.0	192	4	Q9UHA6	Q9uha6 homo sapien
18	155.5	19.0	218	4	Q9NZH6	Q9nzh6 homo sapien
19	155.5	19.0	218	4	Q9HBF3	Q9hbf3 homo sapien
20	154.5	18.9	267	13	O73909	O73909 gallus gall
21	154	18.8	160	11	Q9JLA2	Q9jla2 mus musculu
22	137.5	16.8	267	6	Q29082	Q29082 sus scrofa
23	135.5	16.6	283	13	Q9PVZ5	Q9pvz5 xenopus lae
24	123	15.0	118	6	Q9TSJ0	Q9tsj0 equus cabal
25	120.5	14.7	266	11	Q9WVG1	Q9wvg1 cavia porce
26	113	13.8	266	6	Q9TTK1	Q9ttk1 tursiops tr
27	110	13.4	260	13	Q9YGD3	Q9ygd3 oncorhynchu
28	105	12.8	254	13	Q9PT12	Q9pt12 oncorhynchu
29	104.5	12.8	153	4	O43645	O43645 homo sapien
30	95.5	11.7	65	6	Q9TV37	Q9tv37 equus cabal
31	92.5	11.3	276	13	O57398	O57398 cyprinus ca
32	92.5	11.3	276	13	Q9PW18	Q9pw18 cyprinus ca
33	91.5	11.2	269	6	Q9XS77	Q9xs77 trichosurus
34	89	10.9	3623	4	O60494	O60494 homo sapien
35	84.5	10.3	299	11	Q60800	Q60800 mus musculu
36	84.5	10.3	1313	4	Q9C0C9	Q9c0c9 homo sapien
37	81.5	10.0	272	13	Q9DDF2	Q9ddf2 cyprinus ca
38	80	9.8	381	2	Q9RWJ7	Q9rwj7 deinococcus
39	80	9.8	1092	2	Q54099	Q54099 streptococc
40	78.5	9.6	272	13	Q9DDF3	Q9ddf3 cyprinus ca
41	77.5	9.5	843	6	Q9TUQ3	Q9tuq3 sus scrofa
42	76	9.3	463	10	Q43183	Q43183 solanum tub
43	76	9.3	1117	2	Q53971	Q53971 streptococc
44	75	9.2	64	13	Q98SG5	Q98sg5 scophthalmu
45	73.5	9.0	520	4	O60634	O60634 homo sapien

ALIGNMENTS

RESULT 1
Q9BYX1
ID Q9BYX1 PRELIMINARY; PRT; 144 AA.
AC Q9BYX1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST FKSG75.
GN FKSG75.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Y., Li T., Gong L.;
RT "Identification and characterization of FKSG75, a novel member of the
RT interleukin-1 family.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY026753; AAK01948.1; -.
KW Receptor.
SQ SEQUENCE 144 AA; 15811 MW; 8733B16D6F118BB9 CRC64;

Query Match 72.4%; Score 592; DB 4; Length 144;
Best Local Similarity 98.2%; Pred. No. 8e-55;
Matches 111; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      40 EKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRF 99
           |||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      32 EKICILPNRGLARTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRF 91

Qy     100 TFFQSSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      92 TFFQSSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 144
```

RESULT 2
Q9JIG2
ID Q9JIG2 PRELIMINARY; PRT; 156 AA.
AC Q9JIG2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 DELTA (INTERLEUKIN 1 RECEPTOR ANTAGONIST HOMOLOG 1).
GN   IL1HY1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA   Kastelein R.A.;
RT   "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE, AND STOMACH;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF230378; AAF91275.1; -.
DR   EMBL; AK009741; BAB26471.1; -.
DR   EMBL; AK008977; BAB26002.1; -.
DR   MGD; MGI:1859325; Il1hy1.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ   SEQUENCE   156 AA;  17136 MW;  A4D1EE2F93CF77A7 CRC64;

  Query Match             37.8%;  Score 309;  DB 11;  Length 156;
  Best Local Similarity   45.2%;  Pred. No. 6.3e-25;
  Matches   70;  Conservative   23;  Mismatches   56;  Indels    6;  Gaps    3;

Qy       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
           |  |  |  : :| :  | ||  : ||| |   |:     |:|  :||| || :  |: |
Db       1 MMVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEEISVVPNRALDASLSPVIL 60

Qy      60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
           |:|||:|||:|  ||:|| |:|| ||| ||| | :|:  |||::   |     |:||:||
Db      61 GVQGGSQCLSC-GTEKGPILKLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPG 119

Qy     120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
           ||||   |  |||:||:  |  |     | |||:|
Db     120 WFLCTSPEADQPVRLTQIPEDPAWDAPITDFYFQQ 154


RESULT   3
Q9QYY1
ID   Q9QYY1      PRELIMINARY;      PRT;   155 AA.
AC   Q9QYY1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IL-1L1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).
GN   IL1HY1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Barton J.L., Nicklin M.J.H.;
RT   "IL-1L1: A Novel Member of the Interleukin-1 Gene Family is Expressed
RT   in Trophoblasts and Macrophages.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
DR   EMBL; AJ250429; CAB59831.1; -.
DR   EMBL; AF200495; AAF69251.1; -.
DR   HSSP; P18510; 1ILR.
DR   MGD; MGI:1859325; Il1hy1.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ   SEQUENCE   155 AA;  17004 MW;  A4B1770F2E12533A CRC64;


  Query Match             37.5%;  Score 307;  DB 11;  Length 155;
  Best Local Similarity   47.8%;  Pred. No. 1e-24;
  Matches   66;  Conservative   20;  Mismatches   46;  Indels    6;  Gaps    3;

Qy      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
           | ||  : ||| |   |:     |:|  :||| || :  |: ||:||||:||:|  ||:|
Db      17 KVLYLHNNQLLAGGLHAEKVIKGEEISVVPNRALDASLSPVILGVQGGSQCLSC-GTEKG 75

Qy      77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
           | |:|| ||| ||| | :|:  |||::   |     |:||:||||||   | |||:||:
Db      76 PILKLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTSPEADQPVRLTQ 135

Qy     137 ESEPSA----RTKFYFEQ 150
             | |     | |||:|
Db     136 IPEDPAWDAPITDFYFQQ 153


RESULT   4
Q9UBH0
ID   Q9UBH0      PRELIMINARY;      PRT;   155 AA.
AC   Q9UBH0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   FIL1 DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR
DE   ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
GN   IL1HY1 OR IL1L1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99443727; PubMed=10512743;
```

```
RA   Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA   Drmanac R., Ford J.E.;
RT   "IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene.";
RL   Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20322477; PubMed=10866108;
RA   Mulero J.J., Nelken S.T., Ford J.E.;
RT   "Organization of the Human Interleukin-1 Receptor Antagonist Gene
RT   IL1HY1.";
RL   Immunogenetics 51:425-428(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA   Kastelein R.A.;
RT   "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF201830; AAF25210.1; -.
DR   EMBL; AF186094; AAF02757.1; -.
DR   EMBL; AJ242737; CAB59822.1; -.
DR   EMBL; AJ242738; CAB59823.1; -.
DR   EMBL; AJ271338; CAB67704.1; -.
DR   EMBL; AF216693; AAF76981.1; -.
DR   EMBL; AF230377; AAF91274.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   155 AA;  16962 MW;  B96DB5EFA2612E25 CRC64;
```

```
  Query Match             34.6%;  Score 283;  DB 4;  Length 155;
  Best Local Similarity   45.7%;  Pred. No. 3.5e-22;
  Matches   63;  Conservative   20;  Mismatches   49;  Indels    6;  Gaps    3;

      18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
         | ||  : ||| |   |       |:|  :||| || :  |: ||:||||:||:|   :|
Db    17 KVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGGSQCLSCGVGQE- 75

Qy    77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
         |:| || ||| ||| | :|:  |||::   |     |:||:|||||   |  |||:||:
Db    76 PTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQ 135

Qy   137 ESE----PSARTKFYFEQ 150
            |     :  | |||:|
Db   136 LPENGGWNAPITDFYFQQ 153
```

```
RESULT   5
O70207
ID   O70207      PRELIMINARY;      PRT;   159 AA.
AC   O70207;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTRACELLULAR INTERLEUKIN-1 RECEPTOR ANTAGONIST.
GN   IL1RN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVBXDBA/1 LACJ;
RX   MEDLINE=98209757; PubMed=9550387;
RA   Gabay C., Porter B., Fantuzzi G., Arend W.P.;
RT   "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
RT   and protein expression of intracellular isoform and tissue
RT   distribution of secreted and intracellular IL-1 receptor antagonist in
RT   vivo.";
RL   J. Immunol. 159:5905-5913(1997).
DR   EMBL; AF001795; AAC15251.1; -.
DR   HSSP; P18510; 1IRA.
DR   MGD; MGI:96547; Il1rn.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ   SEQUENCE   159 AA;  17995 MW;  A7CD35D137846222 CRC64;
```

```
  Query Match             31.5%;  Score 257.5;  DB 11;  Length 159;
  Best Local Similarity   44.5%;  Pred. No. 1.7e-19;
  Matches   61;  Conservative   16;  Mismatches   53;  Indels    7;  Gaps    4;

Qy     16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
          :||  | |: ||: |     |    ||| :|   :|   |  |||| ||  ||:| ::
Db     26 NQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 80

Qy     75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
          :   ||||:||| :| |  ||  |||| :|  |     |:|| ||||||   |  :|| |
Db     81 DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 140

Qy    135 TK-ESEPSARTKFYFEQ 150
          |    ||   ||||::
Db    141 TNTPEEPLIVTKFYFQE 157
```

```
RESULT   6
Q9BEH0
ID   Q9BEH0      PRELIMINARY;      PRT;   176 AA.
AC   Q9BEH0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shin I.-S., Youn H.-Y.;
RT   "Molecular cloning of canine interleukin-1 receptor antagonist (IL-
RT   1ra).";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026462; AAK01472.1; -.
KW   Receptor.
SQ   SEQUENCE   176 AA;  19922 MW;  8486CA54A240212B CRC64;
```

```
  Query Match             30.3%;  Score 248;  DB 6;  Length 176;
  Best Local Similarity   39.7%;  Pred. No. 2e-18;
  Matches   60;  Conservative   20;  Mismatches   61;  Indels   10;  Gaps    4;

Qy      2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
          | :   | : :   :||  | |: ||: |     |    ||:  :|          :|||
Db     33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 84

Qy     61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
          | ||  ||||:: :   |||| ||| :| |  ::  ||||  | ||     |:|| |||
```

```
Db     85 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 144

Qy    121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
          |||    |  :|| ||    | :   |||||::
Db    145 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 175


RESULT   7
Q9GMZ4
ID   Q9GMZ4      PRELIMINARY;      PRT;   177 AA.
AC   Q9GMZ4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
GN   IL-1RA.
OS   Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Tursiops.
OX   NCBI_TaxID=9739;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Inoue Y., Itou T., Sakai T.;
RT   "Cloning and Sequencing of a Bottle-Nosed Dolphin Interleukin-1
RT   Receptor Antagonist.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB038268; BAB11806.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Receptor.
SQ   SEQUENCE   177 AA;  19923 MW;  6FD19A06C09B131B CRC64;

  Query Match             30.0%;  Score 245;  DB 6;  Length 177;
  Best Local Similarity   40.4%;  Pred. No. 4.1e-18;
  Matches   61;  Conservative   18;  Mismatches   62;  Indels   10;  Gaps    4;

Qy      2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
          |  :   | : :   :||  | |: ||: |     |    |||  :|          :|||
Db     33 CEMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVPIE-----PHAMFLG 84

Qy     61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
          | ||  |||||:: :   | || ||| :|    ||  || | :| ||     |:|| |||
Db     85 IHGGKLCLACVKSGDEIKLGLEPVNITDLNSSKEEDKRFAFIRSDSGPTTSFESAACPGW 144

Qy    121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
          |||   |  ||| ||   : : : |||||:|
Db    145 FLCTALETDQPVGLTNTPQDAVQVTKFYFQQ 175


RESULT   8
Q9UPC0
ID   Q9UPC0      PRELIMINARY;      PRT;   143 AA.
AC   Q9UPC0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 INTRACELLULAR RECEPTOR ANTAGONIST VARIANT (FRAGMENT).
GN   IL1RN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98183404; PubMed=9514884;
RA   Weissbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.;
RT   "Detection of an interleukin-1 intracellular receptor antagonist mRNA
RT   variant.";
RL   Biochem. Biophys. Res. Commun. 244:91-95(1998).
DR   EMBL; AF043143; AAC39672.1; -.
DR   HSSP; P18510; 1ITN.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Receptor.
FT   NON_TER     143     143
SQ   SEQUENCE   143 AA;  16142 MW;  4CAD6784B890906B CRC64;

  Query Match             29.2%;  Score 238.5;  DB 4;  Length 143;
  Best Local Similarity   40.9%;  Pred. No. 1.6e-17;
  Matches   56;  Conservative   18;  Mismatches   56;  Indels    7;  Gaps    3;

Qy     16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
          :||  | |: ||: |     |    |||  :|          :|||| ||  ||:|||::
Db     10 NQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 64

Qy     75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
          :  |||| ||| :| :  ::  || | :| ||     |:|| ||||||   |  ||| |
Db     65 DETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSL 124

Qy    135 TKESEPSAR-TKFYFEQ 150
          |   :     |||||::
Db    125 TNMPDEGVMVTKFYFQE 141


RESULT   9
Q14628
ID   Q14628      PRELIMINARY;      PRT;   180 AA.
AC   Q14628;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTRACELLULAR IL-1 RECEPTOR ANTAGONIST TYPE II.
GN   IL-1RN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95355865; PubMed=7629520;
RA   Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
RA   Introna M., Mantovani A., Colotta F.;
RT   "Cloning and characterization of a new isoform of the interleukin 1
RT   receptor antagonist.";
RL   J. Exp. Med. 182:623-628(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97146044; PubMed=8992991;
RA   Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA   Arend W.P., Smith M.F. Jr.;
RT   "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT   and inducible regulatory regions.";
RL   J. Immunol. 158:748-755(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Slightom J.L.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X84348; CAA59087.1; -.
DR   EMBL; U65590; AAB92269.1; -.
DR   HSSP; P18510; 1IRP.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ   SEQUENCE   180 AA;  19897 MW;  624A1574C2334229 CRC64;

  Query Match             29.2%;  Score 238.5;  DB 4;  Length 180;
```

```
  Best Local Similarity   40.9%;  Pred. No. 2e-17;
  Matches   56;  Conservative   18;  Mismatches   56;  Indels    7;  Gaps    3;

Qy      16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
           :||  | |: ||: |     |    |||  :|          :|||| ||  ||:||::
Db      47 NQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 101

Qy      75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
           :  |||| ||| :| :  ::  || | :| ||     |:|| ||||||   |  ||| |
Db     102 DETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSL 161

Qy     135 TKESEPSAR-TKFYFEQ 150
           |   :     |||||::
Db     162 TNMPDEGVMVTKFYFQE 178


RESULT  10
Q9GKK2
ID   Q9GKK2      PRELIMINARY;      PRT;   176 AA.
AC   Q9GKK2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Campbell S.E., Nasir L., Argyle D.J., Gault E., Bennett D.;
RT   "Canine IL-1 Receptor Antagonist cDNA Sequence.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF216526; AAG36777.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   176 AA;  19938 MW;  8486CA54A254206B CRC64;


  Query Match             29.1%;  Score 238;  DB 6;  Length 176;
  Best Local Similarity   39.1%;  Pred. No. 2.2e-17;
  Matches   59;  Conservative   20;  Mismatches   62;  Indels   10;  Gaps    4;

Qy       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
           | :   | : :   :||  | |: ||: |     |    ||:  :|          :|||
        33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 84

        61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
           | ||  ||||:: :   |||| ||| :| |  ::  ||||  | ||     |:|| |||
Db      85 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 144

Qy     121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
           |||   |  : | ||   | :   |||||::
Db     145 FLCTALEADRLVSLTNRPEEAMMVTKFYFQK 175


RESULT  11
Q9NZH8
ID   Q9NZH8      PRELIMINARY;      PRT;   169 AA.
AC   Q9NZH8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
GN   IL1E.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200492; AAF69248.1; -.
DR   EMBL; AF206696; AAG35670.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   169 AA;  18721 MW;  F00A9243706F4154 CRC64;


  Query Match             21.7%;  Score 177.5;  DB 4;  Length 169;
  Best Local Similarity   33.6%;  Pred. No. 5.2e-11;
  Matches   44;  Conservative   21;  Mismatches   61;  Indels    5;  Gaps    2;

Qy      20 LYTRDGQLLVGDPVADNCCAEKI----CTLPNRGLDRTKVPIFLGIQGGSRCLACVETEE 75
           ::|  || ||  | :|:     :    |  |         ||:||||    || | :  |
Db      34 VWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGE 93

Qy      76 GPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLT 135
             |:|||::  | :||   |    | |::: :|    ||: |:| ||:   ::  ||: ||
Db      94 QPTLQLKEQKIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIAS-SKRDQPIILT 152

Qy     136 KESEPSARTKF 146
           |   |  | |
Db     153 SELGKSYNTAF 163


RESULT  12
Q9UHA5
ID   Q9UHA5      PRELIMINARY;      PRT;   157 AA.
AC   Q9UHA5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   FIL1 ETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201833; AAF25213.1; -.
DR   HSSP; P10749; 2MIB.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   157 AA;  17702 MW;  7A54F3D7557A3EE3 CRC64;


  Query Match             21.5%;  Score 176;  DB 4;  Length 157;
  Best Local Similarity   36.6%;  Pred. No. 6.8e-11;
  Matches   34;  Conservative   18;  Mismatches   41;  Indels    0;  Gaps    0;
```

```
Qy      57 IFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAA 116
           ::|||:|   || | | :  |:|||:: || :||   :    | || :  ||    :: :
Db      62 VYLGIKGKDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVS 121

Qy     117 WPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
           :||||:       ||: ||||   :  | || :
Db     122 YPGWFIATSTTSGQPIFLTKERGITNNTNFYLD 154


RESULT  13
Q9D6Z6
ID   Q9D6Z6      PRELIMINARY;      PRT;   183 AA.
AC   Q9D6Z6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   2310043N20RIK PROTEIN.
GN   2310043N20RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK009787; BAB26505.1; -.
DR   MGD; MGI:1916927; 2310043N20Rik.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   183 AA;  20878 MW;  A3ACE339FB96F02F CRC64;


  Query Match             21.0%;  Score 172;  DB 11;  Length 183;
  Best Local Similarity   29.2%;  Pred. No. 2.2e-10;
  Matches   40;  Conservative   25;  Mismatches   68;  Indels    4;  Gaps    1;

Qy      17 QKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVP----IFLGIQGGSRCLACVE 72
           |: ::   |  |   | ::|     :  :  |  :   |     :||||:  : |  |||
Db      44 QQMVWVLTGNTLTAVPASNNVKPVILSLIACRDTEFQDVKKGNLVFLGIKNRNLCFCCVE 103

Qy      73 TEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPV 132
            |  |:|||::|:|  |||  :    | |:    ||    ::  :||||:   :  :| :
Db     104 MEGKPTLQLKEVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFIATSSIERQTI 163

Qy     133 QLTKESEPSARTKFYFE 149
           || :      | || |
Db     164 ILTHQRGKLVNTNFYIE 180


RESULT  14
Q9UHA7
ID   Q9UHA7      PRELIMINARY;      PRT;   158 AA.
AC   Q9UHA7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   FIL1 EPSILON.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201831; AAF25211.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   158 AA;  17684 MW;  469AC84306B0E280 CRC64;


  Query Match             20.7%;  Score 169;  DB 4;  Length 158;
  Best Local Similarity   32.0%;  Pred. No. 3.8e-10;
  Matches   40;  Conservative   23;  Mismatches   58;  Indels    4;  Gaps    1;

Qy      26 QLLVGDPVADNCCAEKICTLPNRGLDRTKV----PIFLGIQGGSRCLACVETEEGPSLQL 81
           | |:  |  |       |  :  | ::  :     ||:||: | : || | :  : |:|||
Db      28 QTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQL 87

Qy      82 EDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPS 141
           :: :| :||   |    | |: | ||     |: |:||||:   :|   |: ||:|   :
Db      88 KEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKA 147

Qy     142 ARTKF 146
             | |
Db     148 NTTDF 152


RESULT  15
O77771
ID   O77771      PRELIMINARY;      PRT;    72 AA.
AC   O77771;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST SECRETORY FORM (FRAGMENT).
GN   IL-1RA.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BREED THOROUGHBRED;
RA   Dhar A.K., Thompson M.S., Paradis M.R., Alcivar-Warren A.;
RT   "Molecular Characterization of Equine Interleukin 1 Receptor
RT   Antagonist (IL-1ra) Gene.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF072476; AAC62237.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   72 AA;  8215 MW;  290CC9B9D4C413D9 CRC64;
```

```
  Query Match             20.1%;  Score 164.5;  DB 6;  Length 72;
  Best Local Similarity   51.4%;  Pred. No. 4.4e-10;
  Matches   36;  Conservative    7;  Mismatches   26;  Indels    1;  Gaps    1;

Qy      82 EDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLT-KESEP 140
           | ||| :| |  ||  |||| :|:||     |:|| ||||||   |  :|| || |  |
Db       1 EAVNITDLSKNKEENKRFTFIRSNSGPTTSFESAACPGWFLCTAQEADRPVSLTNKPKES 60

Qy     141 SARTKFYFEQ 150
             |||||::
Db      61 FMVTKFYFQE 70


Search completed: May 10, 2002, 13:53:45
Job time: 118 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 19, 2002, 07:54:55 ; Search time 270.73 Seconds
(without alignments)
6468.632 Million cell updates/sec

Title: US-09-724-583-1
Perfect score: 1020
Sequence: 1 cagggatcagggttccagga.....acctctaaaaaaaaaaaaaa 1020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1020	100.0	1020	22	AAI70234	Human interleukin-
2	1016.8	99.7	1020	22	AAI70235	Interleukin-1 rece
3	991.2	97.2	998	22	AAA89175	Human interleukin-
4	964.4	94.5	1366	22	AAA89176	Human interleukin-
5	964.4	94.5	1366	22	AAA89178	Human interleukin-
6	699.8	68.6	5445	22	AAA89177	Human interleukin-
7	657.6	64.5	744	22	AAI70236	Interleukin-1 rece
8	634.8	62.2	827	22	ABA08991	Human IL-1 delta h
9	455.8	44.7	459	22	AAD11148	Human FIL-1 theta
10	412	40.4	483	22	AAF83868	Human interleukin-
11	368.4	36.1	538	22	AAD11158	Mouse FIL-1 theta
12	335.8	32.9	339	22	AAD11147	Human FIL-1 theta
13	328.4	32.2	459	22	AAI70237	Mouse interleukin-
14	328.4	32.2	459	22	AAA89180	Mouse interleukin-
15	204.4	20.0	4388	22	AAA89179	Mouse interleukin-
16	204.4	20.0	13017	22	AAI70238	Mouse interleukin-
c 17	122.2	12.0	764	22	AAH04444	Human cDNA clone (
18	117.8	11.5	562	22	AAL23955	Human breast cance
19	111.6	10.9	468	20	AAX89431	Mouse interleukin
20	111.6	10.9	468	22	AAF31373	Invention related
21	111.6	10.9	468	22	AAC81700	Murine interleukin
22	111.6	10.9	470	19	AAV71958	Rodent interleukin
23	111.6	10.9	1275	21	AAA09198	Murine IL-1 homolo
24	111.6	10.9	1284	22	AAF27924	Murine IL-IL1 codi
25	111.6	10.9	1360	21	AAZ50811	Murine TANGO-93 cD
26	111.6	10.9	1385	21	AAA51599	Murine IL-1 recept
27	110.8	10.9	468	20	AAX89432	Human interleukin
28	110.8	10.9	468	21	AAA51597	Human IL-1 recepto
29	110.8	10.9	766	21	AAA09193	Human IL-1 homolog
30	110.8	10.9	1025	22	AAD12295	Human interleukin-
31	110.8	10.9	1282	20	AAZ30050	cDNA encoding a hu
32	110.8	10.9	1282	22	AAF31353	Extension of B2HFL
33	110.8	10.9	1323	21	AAZ50812	Human TANGO-93 cDN
34	110.8	10.9	2490	21	AAZ50813	Human TANGO-93 cDN
35	110.8	10.9	2562	22	AAF27921	Human IL-IL1 codin
36	110.8	10.9	2598	22	AAF92133	Human PRO4342 cDNA
37	110.8	10.9	2647	22	AAF31354	Extension of B2HFL
38	110.8	10.9	2648	20	AAZ30051	cDNA encoding a hu
39	108.8	10.7	1183	22	ABA06384	Human cDNA SEQ ID
40	108.8	10.7	1183	22	AAS29640	Human endocrine po
41	108.8	10.7	1183	22	AAI63963	Human polynucleoti
42	108.8	10.7	1183	22	AAS31277	Human cDNA encodin
43	108.8	10.7	1183	22	AAS34773	cDNA encoding nove
44	105.2	10.3	465	21	AAA09194	Human IL-1 homolog
45	105.2	10.3	465	21	AAA09195	Human IL-1 homolog

ALIGNMENTS

RESULT 1
AAI70234
ID AAI70234 standard; cDNA; 1020 BP.
XX
AC AAI70234;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human interleukin-1 receptor antagonist related protein cDNA.
XX
KW Interleukin-1 receptor antagonist related protein; IL-1ra-R; human;
KW inhibitor; antiarthritic; antirheumatic; osteopathic;
KW antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;
KW antileprotic; antibacterial; tuberculostatic; anorectic; metabolic;
KW antiviral; hyperglycaemic; nootropic; antiparkinsonian;
KW antidepressant; anticonvulsive; tranquillizer; vulnerary;
KW antiasthmatic; antipsoriatic; dermatological; cytostatic;
KW nephrotropic; antihaemorrhagic; vasotropic; cardiant;
KW antiatherosclerotic; antiinfertility; ophthalmological;
KW gene therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 64..522
FT /*tag= a
FT variation replace(194,T)
FT /*tag= b
FT variation replace(215,C)
FT /*tag= c
XX
PN WO200142304-A1.

XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32940.
XX
PR 10-DEC-1999; 99US-170191P.
PR 09-MAR-2000; 2000US-188053P.
PR 04-APR-2000; 2000US-194521P.
PR 10-APR-2000; 2000US-195910P.
PR 28-NOV-2000; 2000US-0170191.
XX
PA (AMGE-) AMGEN INC.
XX
PI Saris CM, Giles J, Mu SX, Xia M, Bass MB, Craveiro R;
XX
DR WPI; 2001-648140/74.
DR P-PSDB; AAM50217.
XX
Novel interleukin-1 receptor antagonist-related polypeptide, its
fragment, variant useful for treating rheumatoid arthritis, septicemia,
PT Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
PT uveitis, eczema -
XX
PS Claim 1; Fig 1A-B; 163pp; English.
XX
CC The present sequence is that of cDNA (ATCC PTA 1423) encoding a
CC novel human interleukin-1 receptor antagonist-related polypeptide,
CC IL-1ra-R (see AAM50217), which has interleukin-1 inhibitor
CC activity. The sequence was derived from cDNA clones obtained by
CC PCR and RACE from placenta and foetal scalp cDNA libraries. Also
CC isolated was an IL-1ra-R variant sequence (see AAI70235), which
CC differed from the present sequence at nucleotide positions 194 and
CC 215 (both altering the encoded amino acid sequence), and a splice
CC variant (see AAI70236). The invention provides IL-1ra-R polypeptides
CC and nucleic acids, as well as selective binding agents, vectors, host
CC cells and methods for producing the IL-1ra-R polypeptides. It also
CC provides pharmaceutical compositions and methods for the diagnosis,
CC treatment, amelioration and/or prevention of diseases, disorders
CC and conditions associated with IL-1ra-R, such as those involving
CC immune system dysfunction, infection, weight disorders, neuronal
CC dysfunction, lung, skin, kidney, bone, vascular system, tumour
CC cells, reproductive system, and eye. The nucleic acids are useful
CC in gene therapy, gene mapping, transgenic animal breeding, and as
CC probes and primers.
XX
SQ Sequence 1020 BP; 288 A; 238 C; 267 G; 227 T; 0 other;

Query Match 100.0%; Score 1020; DB 22; Length 1020;
Best Local Similarity 100.0%; Pred. No. 3.8e-299;
Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 cagggatcagggttccaggaactcaggatctgcagtgaggaccagacaccactgattgca 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 cagggatcagggttccaggaactcaggatctgcagtgaggaccagacaccactgattgca 60

Qy     61 ggaatgtgttccctccccatggcaagatactacataattaaaatatgcagaccagaaggct 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ggaatgtgttccctccccatggcaagatactacataattaaaatatgcagaccagaaggct 120

Qy    121 ctatacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ctatacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgca 180

Qy    181 gagaagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 gagaagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctg 240

Qy    241 gggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttcccta 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 gggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttcccta 300

Qy    301 cagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttc 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 cagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttc 360

Qy    361 accttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 accttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggc 420

Qy    421 tggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgag 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgag 480

Qy    481 ccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcgt 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcgt 540

Qy    541 tttagccttgtgccccaaaccaagctcatcctgctcagggtctatggtaggcagaataa 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 tttagccttgtgccccaaaccaagctcatcctgctcagggtctatggtaggcagaataa 600

Qy    601 tgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 tgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatg 660

Qy    661 tccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 tccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctg 720

Qy    721 ggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagag 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagag 780

Qy    781 agaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaacaa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 agaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaacaa 840

Qy    841 atgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 atgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccg 900

Qy    901 gaaggaacacagctcttgacacatggatttcagctcagtgacacccatttcagacttctg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 gaaggaacacagctcttgacacatggatttcagctcagtgacacccatttcagacttctg 960

Qy    961 acctccacaactataaaatataaacttgtgttattgtaaacctctaaaaaaaaaaaaaa 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 acctccacaactataaaatataaacttgtgttattgtaaacctctaaaaaaaaaaaaaa 1020
```

RESULT 2
AAI70235
ID AAI70235 standard; cDNA; 1020 BP.
XX
AC AAI70235;
XX
DT 07-JAN-2002 (first entry)
XX
DE Interleukin-1 receptor antagonist related protein variant cDNA.
XX
KW Interleukin-1 receptor antagonist related protein; IL-1ra-R; human;
KW inhibitor; antiarthritic; antirheumatic; osteopathic;
KW antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;
KW antileprotic; antibacterial; tuberculostatic; anorectic; metabolic;
KW antiviral; hyperglycaemic; nootropic; antiparkinsonian;
KW antidepressant; anticonvulsive; tranquillizer; vulnerary;
KW antiasthmatic; antipsoriatic; dermatological; cytostatic;
KW nephrotropic; antihaemorrhagic; vasotropic; cardiant;
KW antiatherosclerotic; antiinfertility; ophthalmological;
KW gene therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 64..522

```
FT                   /*tag=  a
FT   variation       replace(194,C)
FT                   /*tag=  b
FT   variation       replace(215,A)
FT                   /*tag=  c
XX
PN   WO200142304-A1.
XX
PD   14-JUN-2001.
XX
PF   04-DEC-2000; 2000WO-US32940.
XX
PR   10-DEC-1999;   99US-170191P.
PR   09-MAR-2000; 2000US-188053P.
PR   04-APR-2000; 2000US-194521P.
PR   10-APR-2000; 2000US-195910P.
PR   28-NOV-2000; 2000US-0170191.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Saris CM,  Giles J,  Mu SX,  Xia M,  Bass MB,  Craveiro R;
XX
DR   WPI; 2001-648140/74.
DR   P-PSDB; AAM50218.
XX
PT   Novel interleukin-1 receptor antagonist-related polypeptide, its
PT   fragment, variant useful for treating rheumatoid arthritis, septicemia,
PT   Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
PT   uveitis, eczema  -
XX
PS   Claim 1; Fig 2A-B; 163pp; English.
XX
CC   The present sequence is that of cDNA encoding a novel human
CC   interleukin-1 receptor antagonist-related polypeptide, IL-1ra-R
CC   (see AAM50218), which has interleukin-1 inhibitor activity.  The
CC   sequence was derived from cDNA clones obtained by PCR and RACE from
CC   placenta and foetal scalp cDNA libraries.  Also isolated was an
CC   IL-1ra-R variant sequence (see AAI70234), which differed from the
CC   present sequence at nucleotide positions 194 and 215 (both altering
CC   the encoded amino acid sequence), and a splice variant (see
CC   AAI70236).  The invention provides IL-1ra-R polypeptides and nucleic
CC   acids, as well as selective binding agents, vectors, host cells and
CC   methods for producing the IL-1ra-R polypeptides.  It also provides
CC   pharmaceutical compositions and methods for the diagnosis,
CC   treatment, amelioration and/or prevention of diseases, disorders
CC   and conditions associated with IL-1ra-R, such as those involving
CC   immune system dysfunction, infection, weight disorders, neuronal
CC   dysfunction, lung, skin, kidney, bone, vascular system, tumour
CC   cells, reproductive system, and eye.  The nucleic acids are useful
     in gene therapy, gene mapping, transgenic animal breeding, and as
     probes and primers.

SQ   Sequence 1020 BP; 287 A; 238 C; 267 G; 228 T; 0 other;
```

```
  Query Match             99.7%;  Score 1016.8;  DB 22;  Length 1020;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-298;
  Matches 1018;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cagggatcagggttccaggaactcaggatctgcagtgaggaccagacaccactgattgca 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 cagggatcagggttccaggaactcaggatctgcagtgaggaccagacaccactgattgca 60

Qy     61 ggaatgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggct 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ggaatgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggct 120

Qy    121 ctatacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ctatacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgca 180

Qy    181 gagaagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctg 240
          |||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||||

Db    181 gagaagatctgcatacttcctaacagaggcttggcccgcaccaaggtccccatttttcctg 240

Qy    241 gggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttcccta 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 gggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttcccta 300

Qy    301 cagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttc 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 cagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttc 360

Qy    361 accttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 accttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggc 420

Qy    421 tggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgag 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgag 480

Qy    481 ccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcgt 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcgt 540

Qy    541 tttagccttgtgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataa 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 tttagccttgtgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataa 600

Qy    601 tgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 tgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatg 660

Qy    661 tccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 tccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctg 720

Qy    721 ggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagag 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagag 780

Qy    781 agaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaacaa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 agaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaacaa 840

Qy    841 atgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 atgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccg 900

Qy    901 gaaggaacacagctcttgacacatggatttcagctcagtgacacccatttcagacttctg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 gaaggaacacagctcttgacacatggatttcagctcagtgacacccatttcagacttctg 960

Qy    961 acctccacaactataaaataataaacttgtgttattgtaaacctctaaaaaaaaaaaaaa 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 acctccacaactataaaataataaacttgtgttattgtaaacctctaaaaaaaaaaaaaa 1020
```

```
RESULT   3
AAA89175
ID   AAA89175 standard; cDNA; 998 BP.
XX
AC   AAA89175;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 cDNA.
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ss.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   CDS             54..512
FT                   /*tag=  a
FT                   /note= "encodes AAB19922"
FT   CDS             3..512
FT                   /*tag=  b
FT                   /partial
FT                   /note= "alternative ORF, encodes AAB19923"
FT   variation       replace(125,C)
FT                   /*tag=  c
FT                   /note= "alters codon GAT (Asp) to GAC (Asp),
FT                          specifically claimed in Claim 9"
FT   variation       replace(184,T)
FT                   /*tag=  d
FT                   /note= "alters codon ACA (Thr) to ATA (Ile),
FT                          specifically claimed in Claim 9"
FT   variation       replace(205,C)
FT                   /*tag=  e
FT                   /note= "alters codon GAC (Asp) to GCC (Ala),
FT                          specifically claimed in Claim 9"
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   P-PSDB; AAB19922, AAB19923.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Claim 1; Page 128-130; 158pp; English.
XX
CC   The present sequence is that of the cDNA insert of clone pIL-1HY2
CC   (ATCC PTA-96) encoding human interleukin-1 Hy2 (IL-1 Hy2, see
CC   AAB19922 and AAB19923), a novel member of the interleukin-1 receptor
CC   antagonist family.  The cDNA was obtained from a human foetal skin
CC   cDNA library using standard PCR, SBH sequence signature analysis
CC   and Sanger sequencing techniques.  Sequencing of PCR products from
CC   various cDNA libraries revealed potential polymorphisms at
CC   nucleotides 125 (altering codon GAT to GAC, both Asp), 184
CC   (altering codon ACA for Thr to ATA for Ile) and 205 (altering
CC   codon GAC for Asp to GCC to Ala).  2 Alternative open reading
CC   frames were identified.  The first had an initiating ATG codon at
CC   position 54-56 of the present sequence.  However, a predicted cDNA
CC   sequence (see AAA89178) based on IL-1 Hy2 genomic DNA contained a C
CC   to T change that resulted in an alternative upstream initiating
CC   methionine which extended the open reading frame.  The IL-1 Hy2
CC   polypeptides and polynucleotides are used to treat cancers
CC   involving elevated levels of IL-1, such as breast adenocarcinoma,
CC   brain tumours, melanoma, giant cell tumours of bone, acute
CC   myelogenous leukaemia, oral epidermoid carcinoma or squamous cell
CC   carcinoma, and inflammatory disease mediated by interleukin-18 (all
CC   claimed).  They can also be used to diagnose, prevent or treat
CC   shock, thrombosis, acute pancreatitis, arthritis, vasculitis,
CC   lupus, immune complex glomerulonephritis, pancreatic cell damage,
CC   allograft and xenograft transplantation, graft versus host disease,
CC   inflammatory bowel disease, bone degenerative diseases, diabetes
CC   and neurodegenerative disorders.  The polynucleotides are also
CC   useful for the design of hybridization probes and PCR primers, in
CC   chromosome and gene mapping, in the recombinant production of
CC   IL-1 Hy2 protein, and in the generation of antisense DNA or RNA.
XX
```

```
SQ   Sequence 998 BP; 271 A; 236 C; 264 G; 227 T; 0 other;

  Query Match             97.2%;  Score 991.2;  DB 22;  Length 998;
  Best Local Similarity   99.7%;  Pred. No. 2.1e-290;
  Matches  993;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      11 ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 60

Qy      71 ccctccccatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ccctccccatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa 120

Qy     131 gagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatct 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatct 180

Qy     191 gcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctggggatccagg 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 gcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctggggatccagg 240

Qy     251 gagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggagg 310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 gagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacagctggagg 300

Qy     311 atgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttcc 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 atgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttcc 360

Qy     371 agagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgt 430
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 agagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctggttcctgt 420

Qy     431 gtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccctcagccc 490
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccctcagccc 480

Qy     491 gtaccaagttttactttgaacagagctggtagggagacaggaaactgcgttttagccttg 550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 gtaccaagttttactttgaacagagctggtagggagacaggaaactgcgttttagccttg 540

Qy     551 tgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccga 610
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 tgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataatgtcccccga 600

Qy     611 aatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtccaaagagg 670
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 aatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgtccaaagagg 660

Qy     671 ttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatcctt 730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatcctt 720

Qy     731 gtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaag 790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 gtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagagagaatggaag 780

Qy     791 ataccatgcttctaattttgaagatggagtgaggggccttgagccaacaaatgcaggtgt 850
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     781 ataccatgcttctaattttgaagatggagtgaggggccttgagccaacatatgcaggtgt 840

Qy     851 ttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaaggaacac 910
           |||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||||
Db     841 ttttagaaggaggaaaagccaagggaacggattctcctctatagtctccggaaggaacac 900

Qy     911 agctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctccacaa 970
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 agctcttgacacatggatttcagctcagtgacacccatttcagacttctgacctccacaa 960

Qy     971 ctataaaataataaacttgtgttattgtaaacctct 1006
           |||||||||||||||||||||||||||||||||||
```

```
Db    961 ctataaaataataaacttgtgttattgtaaacctct 996


RESULT   4
AAA89176
ID   AAA89176 standard; cDNA; 1366 BP.
XX
AC   AAA89176;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 cDNA.
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             422..880
FT                   /*tag= a
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   P-PSDB; AAB19922.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Claim 1; Page 145-146; 158pp; English.
XX
CC   The present sequence is that of cDNA encoding human interleukin-1
CC   Hy2 (IL-1 Hy2, see AAB19922), a novel member of the interleukin-1
CC   receptor antagonist family. The sequence was obtained following
CC   resequencing of cDNA clone pIL-1Hy2 (see AAA89175), extending the 5'
CC   sequence. An alternative IL-1 Hy2 cDNA sequence (see AAA89178),
CC   predicted from the IL-1 Hy2 genomic DNA, contains a C to T
CC   nucleotide change at position 279, which generates an alternative
CC   upstream initiating methionine for open reading frame encoding a
CC   200-amino acid protein (see AAB18824). IL-1 Hy2 polypeptides and
CC   polynucleotides are used to treat cancers involving elevated levels
CC   of IL-1, such as breast adenocarcinoma, brain tumours, melanoma,
CC   giant cell tumours of bone, acute myelogenous leukaemia, oral
CC   epidermoid carcinoma or squamous cell carcinoma, and inflammatory
CC   disease mediated by interleukin-18 (all claimed). They can also be
CC   used to diagnose, prevent or treat shock, thrombosis, acute
CC   pancreatitis, arthritis, vasculitis, lupus, immune complex
CC   glomerulonephritis, pancreatic cell damage, allograft and xenograft
CC   transplantation, graft versus host disease, inflammatory bowel
CC   disease, bone degenerative diseases, diabetes and neurodegenerative
CC   disorders. The polynucleotides are also useful for the design of
CC   hybridization probes and PCR primers, in chromosome and gene
CC   mapping, in the recombinant production of IL-1 Hy2 protein, and in
CC   the generation of antisense DNA or RNA.
XX
SQ   Sequence 1366 BP; 334 A; 350 C; 368 G; 314 T; 0 other;


  Query Match           94.5%;  Score 964.4;  DB 22;  Length 1366;
  Best Local Similarity 99.4%;  Pred. No. 3.4e-282;
  Matches  968;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     33 cagtgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagatacta 92
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 cagtgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagatacta 450

Qy     93 cataattaaatatgcagaccagaaggctctatacacaagagatggccagctgctggtggg 152
        |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    451 cataattaaatatgcagaccagaaggctctatacacaagagacggccagctgctggtggg 510

Qy    153 agatcctgttgcagacaactgctgtgcagagaagatctgcacacttcctaacagaggctt 212
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 agatcctgttgcagacaactgctgtgcagagaagatctgcacacttcctaacagaggctt 570

Qy    213 ggaccgcaccaaggtccccatttttcctggggatccagggagggagccgctgcctggcatg 272
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 ggaccgcaccaaggtccccatttttcctggggatccagggagggagccgctgcctggcatg 630

Qy    273 tgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaactgta 332
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 tgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaactgta 690

Qy    333 caaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgcctt 392
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 caaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgcctt 750

Qy    393 caggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagccccagca 452
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 caggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagccccagca 810

Qy    453 gccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttactttgaaca 512
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 gccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttactttgaaca 870

Qy    513 gagctggtagggagacaggaaactgcgttttagccttgtgccccaaaccaagctcatcc 572
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 gagctggtagggagacaggaaactgcgttttagccttgtgccccaaaccaagctcatcc 930

Qy    573 tgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaatccc 632
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 tgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaatccc 990

Qy    633 aagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgtta 692
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 aagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgtta 1050

Qy    693 aggatcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag 752
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 aggatcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag 1110

Qy    753 aaggaggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaa 812
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 aaggaggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaa 1170

Qy    813 gatggagtgaggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaa 872
        |||||||||||||||||||||||||| ||||  ||||||||||||| ||||||||||
Db   1171 gatggagtgaggggccttgagccaacatatgcttgtgtttttagaaggaggaaaagccaa 1230

Qy    873 gggaacggattctcctctagagtctccggaaggaacacagctcttgacacatggatttca 932
        |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1231 gggaacggattctcctctatagtctccggaaggaacacagctcttgacacatggatttca 1290

Qy    933 gctcagtgacacccatttcagacttctgacctccacaactataaaataataaacttgtgt 992
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 gctcagtgacacccatttcagacttctgacctccacaactataaaataataaacttgtgt 1350

Qy    993 tattgtaaacctct 1006
        ||||||||||||||
Db   1351 tattgtaaacctct 1364
```

```
RESULT   5
AAA89178
ID   AAA89178 standard; cDNA; 1366 BP.
XX
AC   AAA89178;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 cDNA (alternative ORF).
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ss.
XX
OS   Homo sapiens.
XX
FT   Key             Location/Qualifiers
FT   CDS             278..880
FT                   /*tag= a
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   P-PSDB; AAB19924.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Claim 1; Page 143; 158pp; English.
XX
CC   The present sequence is that of cDNA encoding human interleukin-1
CC   Hy2 (IL-1 Hy2, see AAB19924), a novel member of the interleukin-1
CC   receptor antagonist family.  The sequence was deduced from isolated
CC   IL-1 Hy2 genomic DNA (see AAA89177).  It contains thymidine at
CC   nucleotide 279, whereas IL-1 Hy2 cDNA obtained by PCR amplification
CC   (see AAA89176) has cytosine at this position.  The C to T change
CC   extends the IL-1 Hy2 open reading frame in the 5' direction,
CC   resulting in a 200-amino acid protein, while the amplified cDNA
CC   encodes a 152-amino acid protein (see AAB19922).  However, sequences
CC   surrounding the translation initiation codon at nucleotide 422 of
CC   the present sequence are more similar to the Kozak translation
CC   start site consensus than the sequences surrounding nucleotide 278,
CC   suggesting that IL-1 Hy2 is encoded by the shorter open reading
CC   from.  IL-1 Hy2 polypeptides and polynucleotides are used to treat
CC   cancers involving elevated levels of IL-1, such as breast
CC   adenocarcinoma, brain tumours, melanoma, giant cell tumours of
CC   bone, acute myelogenous leukaemia, oral epidermoid carcinoma or
CC   squamous cell carcinoma, and inflammatory disease mediated by
CC   interleukin-18 (all claimed).  They can also be used to diagnose,
CC   prevent or treat shock, thrombosis, acute pancreatitis, arthritis,
CC   vasculitis, lupus, immune complex glomerulonephritis, pancreatic
CC   cell damage, allograft and xenograft transplantation, graft versus
CC   host disease, inflammatory bowel disease, bone degenerative
CC   diseases, diabetes and neurodegenerative disorders.  The
CC   polynucleotides are also useful for the design of hybridization
CC   probes and PCR primers, in chromosome and gene mapping, in the
CC   recombinant production of IL-1 Hy2 protein, and in the generation
CC   of antisense DNA or RNA.
XX
SQ   Sequence 1366 BP; 334 A; 349 C; 368 G; 315 T; 0 other;

  Query Match             94.5%;  Score 964.4;  DB 22;  Length 1366;
  Best Local Similarity   99.4%;  Pred. No. 3.4e-282;
  Matches  968;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      33 cagtgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagatacta 92
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 cagtgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagatacta 450

Qy      93 cataattaaatatgcagaccagaaggctctatacacaagagatggccagctgctggtggg 152
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     451 cataattaaatatgcagaccagaaggctctatacacaagagacggccagctgctggtggg 510

Qy     153 agatcctgttgcagacaactgctgtgcagagaagatctgcacacttcctaacagaggctt 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 agatcctgttgcagacaactgctgtgcagagaagatctgcacacttcctaacagaggctt 570

Qy     213 ggaccgcaccaaggtccccatttttcctggggatccagggagggagccgctgcctggcatg 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571 ggaccgcaccaaggtccccatttttcctggggatccagggagggagccgctgcctggcatg 630

Qy     273 tgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaactgta 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631 tgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaactgta 690

Qy     333 caaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgcctt 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 caaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgcctt 750

Qy     393 caggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagccccagca 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 caggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagccccagca 810

Qy     453 gccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttactttgaaca 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 gccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttactttgaaca 870

Qy     513 gagctggtagggagacaggaaactgcgttttagccttgtgccccaaaccaagctcatcc 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 gagctggtagggagacaggaaactgcgttttagccttgtgccccaaaccaagctcatcc 930

Qy     573 tgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaatccc 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 tgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaatccc 990

Qy     633 aagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgtta 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     991 aagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgtta 1050

Qy     693 aggatcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag 752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 aggatcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag 1110

Qy     753 aaggaggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaa 812
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1111 aaggaggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaa 1170

Qy     813 gatggagtgaggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaa 872
           |||||||||||||||||||||||| ||||  |||||||||||||| ||||||||||||
Db    1171 gatggagtgaggggccttgagccaacatatgcttgtgtttttagaaggaggaaaagccaa 1230

Qy     873 gggaacggattctcctctagagtctccggaaggaacacagctcttgacacatggatttca 932
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    1231 gggaacggattctcctctatagtctccggaaggaacacagctcttgacacatggatttca 1290

Qy     933 gctcagtgacacccatttcagacttctgacctccacaactataaaataataaacttgtgt 992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1291 gctcagtgacacccatttcagacttctgacctccacaactataaaataataaacttgtgt 1350

Qy     993 tattgtaaacctct 1006
```

```
          ||||||||||||||
Db   1351 tattgtaaacctct 1364


RESULT   6
AAA89177
ID   AAA89177 standard; DNA; 5445 BP.
XX
AC   AAA89177;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human interleukin-1 Hy2 gene.
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ds.
XX
OS   Homo sapiens.

     Key             Location/Qualifiers
FT   CDS             2188..4961
FT                   /*tag= a
FT                   /note = "contains introns"
FT   exon            1911..2363
FT                   /*tag= b
FT                   /number = 1
FT   intron          2364..3924
FT                   /*tag= c
FT                   /number = 1
FT   exon            3925..4011
FT                   /*tag= d
FT                   /number = 2
FT   intron          4012..4318
FT                   /*tag= e
FT                   /number = 2
FT   exon            4320..4447
FT                   /*tag= f
FT                   /number = 3
FT   intron          4448..4747
FT                   /*tag= g
FT                   /number = 3
FT   exon            4749..5445
FT                   /*tag= h
FT                   /number = 4
XX
PN   WO200071719-A1.

     30-NOV-2000.

PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   P-PSDB; AAB19924.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Example 8; Page 146-149; 158pp; English.
XX
CC   The present sequence is that of human genomic DNA encoding
CC   interleukin-1 Hy2 (IL-1 Hy2, see AAB19924), a novel member
CC   of the interleukin-1 receptor antagonist family.  The DNA was
CC   obtained by screening a commercial human BAC library with IL-1 Hy2
CC   cDNA.  Exons were predicted using GenScan software.  The predicted
CC   cDNA (see AAA89178) based on this genomic sequence contains thymidine
CC   at nucleotide 279, whereas IL-1 Hy2 cDNA obtained by PCR
CC   amplification (see AAA89176) contains cytosine at this position.  The
CC   change in nucleotides extends the IL-1 Hy2 open reading frame in the
CC   5' direction, resulting in a 200-amino acid polypeptide, whereas the
CC   amplified cDNA encodes a 152-amino acid polypeptide (see AAB19922).
CC   IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers
CC   involving elevated levels of IL-1, such as breast adenocarcinoma,
CC   brain tumours, melanoma, giant cell tumours of bone, acute
CC   myelogenous leukaemia, oral epidermoid carcinoma or squamous cell
CC   carcinoma, and inflammatory disease mediated by interleukin-18 (all
CC   claimed).  They can also be used to diagnose, prevent or treat
CC   shock, thrombosis, acute pancreatitis, arthritis, vasculitis,
CC   lupus, immune complex glomerulonephritis, pancreatic cell damage,
CC   allograft and xenograft transplantation, graft versus host disease,
CC   inflammatory bowel disease, bone degenerative diseases, diabetes
CC   and neurodegenerative disorders.  The polynucleotides are also
CC   useful for the design of hybridization probes and PCR primers, in
CC   chromosome and gene mapping, in the recombinant production of
CC   IL-1 Hy2 protein, and in the generation of antisense DNA or RNA.
XX
SQ   Sequence 5445 BP; 1365 A; 1382 C; 1246 G; 1452 T; 0 other;


  Query Match             68.6%;  Score 699.8;  DB 22;  Length 5445;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-201;
  Matches  704;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     296 ccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacac 355
           || | |  |   ||||||||||||||||||||||||||||||||||||||||||||||||
Db    4735 ccttgcccccacaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacac 4794

Qy     356 gcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggc 415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4795 gcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggc 4854

Qy     416 ctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggaga 475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4855 ctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggaga 4914

Qy     476 gtgagccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaac 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4915 gtgagccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaac 4974

Qy     536 tgcgttttagccttgtgcccccaaaccaagctcatcctgctcagggtctatggtaggcag 595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4975 tgcgttttagccttgtgcccccaaaccaagctcatcctgctcagggtctatggtaggcag 5034

Qy     596 aataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccat 655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5035 aataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccat 5094

Qy     656 acatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaa 715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5095 acatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaa 5154

Qy     716 tcctgggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtca 775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5155 tcctgggttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtca 5214

Qy     776 gagagagaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagcc 835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5215 gagagagaatggaagataccatgcttctaattttgaagatggagtgaggggccttgagcc 5274

Qy     836 aacaaatgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagt 895
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5275 aacaaatgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagt 5334

Qy     896 ctccggaaggaacacagctcttgacacatggatttcagctcagtgacacccatttcagac 955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5335 ctccggaaggaacacagctcttgacacatggatttcagctcagtgacacccatttcagac 5394
```

```
Qy     956 ttctgacctccacaactataaaataataaacttgtgttattgtaaaccctct 1006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5395 ttctgacctccacaactataaaataataaacttgtgttattgtaaaccctct 5445


RESULT   7
AAI70236
ID   AAI70236 standard; cDNA; 744 BP.
XX
AC   AAI70236;
XX
DT   07-JAN-2002  (first entry)
XX
DE   Interleukin-1 receptor antagonist related protein splice variant.
XX
KW   Interleukin-1 receptor antagonist related protein; IL-1ra-R; human;
KW   inhibitor; antiarthritic; antirheumatic; osteopathic;
KW   antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;
KW   antileprotic; antibacterial; tuberculostatic; anorectic; metabolic;
KW   antiviral; hyperglycaemic; nootropic; antiparkinsonian;
KW   antidepressant; anticonvulsive; tranquillizer; vulnerary;
KW   antiasthmatic; antipsoriatic; dermatological; cytostatic;
KW   nephrotropic; antihaemorrhagic; vasotropic; cardiant;
KW   antiatherosclerotic; antiinfertility; ophthalmological;
KW   gene therapy; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             58..573
FT                   /*tag=  a
XX
PN   WO200142304-A1.
XX
PD   14-JUN-2001.
XX
PF   04-DEC-2000; 2000WO-US32940.
XX
PR   10-DEC-1999;   99US-170191P.
PR   09-MAR-2000; 2000US-188053P.
PR   04-APR-2000; 2000US-194521P.
PR   10-APR-2000; 2000US-195910P.
PR   28-NOV-2000; 2000US-0170191.
XX
PA   (AMGE-) AMGEN INC.

     Saris CM,  Giles J,  Mu SX,  Xia M,  Bass MB,  Craveiro R;

DR   WPI; 2001-648140/74.
DR   P-PSDB; AAM50219.
XX
PT   Novel interleukin-1 receptor antagonist-related polypeptide, its
PT   fragment, variant useful for treating rheumatoid arthritis, septicemia,
PT   Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
PT   uveitis, eczema  -
XX
PS   Claim 1; Fig 3; 163pp; English.
XX
CC   The present sequence is that of cDNA encoding a splice variant (see
CC   AAM50219) of human interleukin-1 receptor antagonist-related
CC   polypeptide IL-1ra-R, a novel protein that has interleukin-1
CC   inhibitor activity.  The sequence was obtained from a human
CC   placenta cDNA library by PCR amplification.  The splice variant
CC   may arise from splicing (or a fusion) of the first 2 exons of
CC   the upstream IL-1 Omega gene onto the second exon of the IL-1ra-R
CC   gene.  The invention provides IL-1ra-R polypeptides and nucleic
CC   acids, as well as selective binding agents, vectors, host cells
CC   and methods for producing the IL-1ra-R polypeptides.  It also
CC   provides pharmaceutical compositions and methods for the diagnosis,
CC   treatment, amelioration and/or prevention of diseases, disorders
CC   and conditions associated with IL-1ra-R, such as those involving
CC   immune system dysfunction, infection, weight disorders, neuronal
CC   dysfunction, lung, skin, kidney, bone, vascular system, tumour
CC   cells, reproductive system, and eye.  The nucleic acids are useful
CC   in gene therapy, gene mapping, transgenic animal breeding, and as
CC   probes and primers.
XX
SQ   Sequence 744 BP; 183 A; 194 C; 205 G; 162 T; 0 other;


  Query Match             64.5%;  Score 657.6;  DB 22;  Length 744;
  Best Local Similarity   99.4%;  Pred. No. 3.6e-189;
  Matches  660;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      30 ctgcagtgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagata 89
           || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 cttccgtgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagata 140

Qy      90 ctacataattaaatatgcagaccagaaggctctatacacaagagatggccagctgctggt 149
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 ctacataattaaatatgcagaccagaaggctctatacacaagagatggccagctgctggt 200

Qy     150 gggagatcctgttgcagacaactgctgtgcagagaagatctgcacacttcctaacagagg 209
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     201 gggagatcctgttgcagacaactgctgtgcagagaagatctgcatacttcctaacagagg 260

Qy     210 cttggaccgcaccaaggtccccatttttcctggggatccagggagggagccgctgcctggc 269
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 cttggcccgcaccaaggtccccatttttcctggggatccagggagggagccgctgcctggc 320

Qy     270 atgtgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaact 329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 atgtgtggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaact 380

Qy     330 gtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgc 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 gtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgc 440

Qy     390 cttcaggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagcccca 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     441 cttcaggcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagcccca 500

Qy     450 gcagccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttacttttga 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     501 gcagccagtacagctcaccaaggagagtgagccctcagcccgtaccaagttttacttttga 560

Qy     510 acagagctggtagggagacaggaaactgcgttttagccttgtgccccccaaaccaagctca 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     561 acagagctggtagggagacaggaaactgcgttttagccttgtgccccccaaaccaagctca 620

Qy     570 tcctgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaat 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     621 tcctgctcagggtctatggtaggcagaataatgtcccccgaaatatgtccacatcctaat 680

Qy     630 cccaagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatg 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     681 cccaagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatg 740

Qy     690 ttaa 693
           ||||
Db     741 ttaa 744


RESULT   8
ABA08991
ID   ABA08991 standard; cDNA; 827 BP.
XX
AC   ABA08991;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human IL-1 delta homologue-encoding cDNA, SEQ ID NO:767.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
```

```
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US03800.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   P-PSDB; ABB11747.
XX
PT   Human proteins and DNA encoding sequences useful for preventing,
PT   treating or ameliorating a medical condition in a mammalian subject
PT   e.g. arthritis and cancer -
XX
PS   Claim 1; Page 686; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
     immunomodulatory activity; activin- or inhibin-related activities;
     chemotactic or chemokinetic activities; haemostatic, thrombotic or
     thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a cDNA encoding a
CC   novel human polypeptide of the invention.
XX
SQ   Sequence 827 BP; 164 A; 175 C; 192 G; 129 T; 167 other;

  Query Match             62.2%;  Score 634.8;  DB 22;  Length 827;
  Best Local Similarity   79.0%;  Pred. No. 3.2e-182;
  Matches  636;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy      2 agggatcagggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcag 61
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     23 acggatcagggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcag 82

Qy     62 gaatgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctc 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     83 gaatgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctc 142

Qy    122 tatacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcag 181
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    143 tatacacaagagacggccagctgctggtgggagatcctgttgcagacaactgctgtgcag 202

Qy    182 agaagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctgg 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    203 agaagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctgg 262

Qy    242 ggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctac 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 ggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctac 322

Qy    302 agctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttca 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 agctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttca 382

Qy    362 ccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggct 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    383 ccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggct 442

Qy    422 ggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagc 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    443 ggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagc 502

Qy    482 cctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcgtt 541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    503 cctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaactgcgtt 562

Qy    542 ttagccttgtgcccccaaaccaagctcatcctgctcagggtctatggtaggcagaataat 601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    563 ttagccttgtgcccccaaaccaagctcatcctgctcagggtctannnnnnnnnnnnnnnn 622

Qy    602 gtcccccgaaatatgtccacatcctaatcccaagatctgtgcatatgttaccatacatgt 661

Db    623 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 682

Qy    662 ccaaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctgg 721

Db    683 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 742

Qy    722 gttatccttgtgggctcagtttaatcacaagaaggaggcaggaagggagagtcagagaga 781
                                          ||||||||||||||||||||||||||||
Db    743 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnaaggaggcaggaagggagagtcagagaga 802

Qy    782 gaatggaagataccatgcttctaat 806
          |||||||||||||||||||||||||
Db    803 gaatggaagataccatgcttctaat 827


RESULT   9
AAD11148
ID   AAD11148 standard; DNA; 459 BP.
XX
AC   AAD11148;
XX
DT   24-SEP-2001  (first entry)
XX
```

```
DE   Human FIL-1 theta full-length DNA.
XX
KW   Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;
KW   insulin dependent diabetes mellitus; lymphoma; microbial infection;
KW   ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;
KW   tibial muscular dystrophy; inflammation; gene therapy; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..459
FT                   /*tag= a
FT                   /product= "Human FIL-1 theta full-length protein"
FT   variation       replace (131, T)
FT                   /*tag= b
FT                   /note= "This polymorphism results in an amino
FT                   acid change from Thr to Ile at position 44"
FT   variation       replace (131..132, TC)
FT                   /*tag= b
FT                   /note= "This polymorphism results in an amino
FT                   acid change from Thr to Ile at position 44"
FT   variation       replace (152, C)
FT                   /*tag= b
FT                   /note= "This polymorphism results in an amino
FT                   acid change from Asp to Ala at position 51"
XX
PN   WO200155211-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02514.
XX
PR   27-JAN-2000; 2000US-0178389.
PR   11-APR-2000; 2000US-0195962.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE;
XX
DR   WPI; 2001-457718/49.
DR   P-PSDB; AAE05840.
XX
PT   isolated FIL-1 theta polypeptide to induce or inhibit the induction of
PT   fever and to stimulate the immune system for the treatment of microbial
PT   infections -
XX

     Claim 1; Page 5; 65pp; English.

     The invention relates to interleukin-1 (IL-1) family ligand designated
CC   as FIL-1 theta polypeptides and nucleic acid molecules encoding such
CC   polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin
CC   dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/
CC   lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1
CC   theta polypeptides are used to activate and/or inhibit the activation
CC   of vascular endothelial cells and lymphocytes; the induction of local
CC   tissue destruction and fever; the stimulation of macrophages and
CC   vascular endothelial cells to produce IL-6 and the induction of
CC   prostaglandins. They are also used to treat inflammation and microbial
CC   infections. FIL-1 theta DNA is useful in antisense therapy and gene
CC   therapy. The present sequence is a DNA encoding human FIL-1 theta
CC   full-length protein.
XX
SQ   Sequence 459 BP; 109 A; 124 C; 132 G; 94 T; 0 other;


  Query Match             44.7%;  Score 455.8;  DB 22;  Length 459;
  Best Local Similarity   99.6%;  Pred. No. 5.2e-128;
  Matches  457;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      64 atgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctcta 123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 atgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctcta 60

Qy     124 tacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagag 183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 tacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagag 120

Qy     184 aagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttcctgggg 243
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 aagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttcctgggg 180

Qy     244 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag 303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag 240

Qy     304 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc 363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc 300

Qy     364 ttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctgg 423
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     301 ttcttccagagcagctcaggctccgccttcaggcttgaggccgctgcctggcctggctgg 360

Qy     424 ttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccc 483
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     361 ttcctgtgtggcccggcagagccccagcagccagtacagctcactaaggagagtgagccc 420

Qy     484 tcagcccgtaccaagttttactttgaacagagctggtag 522
           |||||||||||||||||||||||||||||||||||||||
Db     421 tcagcccgtaccaagttttactttgaacagagctggtag 459


RESULT  10
AAF83868
ID   AAF83868 standard; cDNA; 483 BP.
XX
AC   AAF83868;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human interleukin-1 receptor antagonist (NOVINTRA A) encoding cDNA.
XX
KW   NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW   gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW   cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW   antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW   antiasthmatic; antiallergic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..467
FT                   /*tag= a
FT                   /product= "NOVINTRA A"
XX
PN   WO200140291-A2.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US33029.
XX
PR   06-DEC-1999;   99US-0169056.
PR   09-DEC-1999;   99US-0169866.
PR   09-DEC-1999;   99US-0169886.
PR   10-DEC-1999;   99US-0170252.
PR   12-JAN-2000; 2000US-0175740.
PR   05-DEC-2000; 2000US-0170252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess CE,  Prayaga SK,  Shimkets RA,  Rastelli L,  Zerhusen BD;
PI   Mezes PS;
XX
DR   WPI; 2001-374790/39.
DR   P-PSDB; AAB84999.
XX
```

```
PT   Novel isolated human transmembrane, neuromedin peptide
PT   gonadotropin-like protein and interleukin-1 receptor antagonist
PT   proteins, useful for treating cancer, immune response disorder,
PT   metabolic function disorders -
XX
PS   Claim 8; Fig 9A; 138pp; English.
XX
CC   The invention provides novel polypeptides (NOVX) selected from human
CC   transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC   gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC   antagonist proteins (NOVINTRA A and B). The invention also provides
CC   methods in which a NOVX polypeptide, polynucleotide and antibody are
CC   used in the detection, prevention and treatment of a broad range of
CC   pathological states. NOVTRAN can be used to treat is a cell signaling
CC   disorder such as cancer, immune response disorder, hematopoietic
CC   disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC   endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC   central nervous system, breast, colon, ovary, kidney, prostate and
CC   thyroid. NOVGON can be used to treat reproductive development disorder,
CC   metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC   to treat bone metabolism or structure disorder, inflammatory response
CC   disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC   arthritis and cancer. The present sequence represents a cDNA encoding
CC   the NOVINTRA A polypeptide.
XX
SQ   Sequence 483 BP; 114 A; 134 C; 138 G; 97 T; 0 other;
```

```
  Query Match             40.4%;  Score 412;  DB 22;  Length 483;
  Best Local Similarity   93.5%;  Pred. No. 1.1e-114;
  Matches  449;  Conservative    0;  Mismatches   10;  Indels   21;  Gaps    1;

Qy      80 tggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcc 139
           || ||    |  | || ||||||||||||||||||||||||||||||||||||||||||
Db       4 tgtcatactgtttcagaattaaatatgcagaccagaaggctctatacacaagagatggcc 63

Qy     140 agctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatctgcacacttc 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      64 agctgctggtgggagatcctgttgcagacaactgctgtgcagagaagatctgcatacttc 123

Qy     200 ctaacagaggcttggaccgcaccaaggtccccatttcctggggatccagggagggagcc 259
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     124 ctaacagaggcttggcccgcaccaaggtccccattttcctggggatccagggagggagcc 183

Qy     260 gctgcctggcatgtgtggagacagaagaggggccttccctacagctgg------------ 307
           |||||||||||||||||||||||||||||||||||||||||||||
Db     184 gctgcctggcatgtgtggagacagaagaggggccttccctacagctggagccatccacct 243

Qy     308 ---------aggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgct 358
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||
       244 tgcccccacaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgct 303

Qy     359 tcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctg 418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 tcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctg 363

Qy     419 gctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtg 478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 gctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtg 423

Qy     479 agccctcagcccgtaccaagttttacttttgaacagagctggtagggagacaggaaactgc 538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 agccctcagcccgtaccaagttttacttttgaacagagctggtagggagacaggaaactgc 483
```

```
RESULT  11
AAD11158
ID   AAD11158 standard; DNA; 538 BP.
XX
AC   AAD11158;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Mouse FIL-1 theta DNA.
XX
KW   Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;
KW   insulin dependent diabetes mellitus; lymphoma; microbial infection;
KW   ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;
KW   tibial muscular dystrophy; inflammation; gene therapy; mouse; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             29..487
FT                   /*tag=  a
FT                   /product= "Mouse FIL-1 theta protein"
XX
PN   WO200155211-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02514.
XX
PR   27-JAN-2000; 2000US-0178389.
PR   11-APR-2000; 2000US-0195962.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE;
XX
DR   WPI; 2001-457718/49.
DR   P-PSDB; AAE05841.
XX
PT   isolated FIL-1 theta polypeptide to induce or inhibit the induction of
PT   fever and to stimulate the immune system for the treatment of microbial
PT   infections -
XX
PS   Claim 1; Page 5-6; 65pp; English.
XX
CC   The invention relates to interleukin-1 (IL-1) family ligand designated
CC   as FIL-1 theta polypeptides and nucleic acid molecules encoding such
CC   polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin
CC   dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/
CC   lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1
CC   theta polypeptides are used to activate and/or inhibit the activation
CC   of vascular endothelial cells and lymphocytes; the induction of local
CC   tissue destruction and fever; the stimulation of macrophages and
CC   vascular endothelial cells to produce IL-6 and the induction of
CC   prostaglandins. They are also used to treat inflammation and microbial
CC   infections. FIL-1 theta DNA is useful in antisense therapy and gene
CC   therapy. The present sequence is a DNA encoding mouse FIL-1 theta
CC   protein.
XX
SQ   Sequence 538 BP; 132 A; 148 C; 140 G; 118 T; 0 other;
```

```
  Query Match             36.1%;  Score 368.4;  DB 22;  Length 538;
  Best Local Similarity   80.3%;  Pred. No. 2e-101;
  Matches  432;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy      36 tgaggaccagacaccactgattgcaggaatgtgttccctccccatggcaagatactacat 95
           ||| ||||||||||  |  | |||||||||||| ||||| ||||||||||||||||||||
Db       1 tgaagaccagacactcccaactgcaggaatgtgctcccttcccatggcaagatactacat 60

Qy      96 aattaaatatgcagaccagaaggctctatacacaagagatggccagctgctggtgggaga 155
           ||| ||  ||||| | || |||||| | |||||| |  |||||||||| ||| |||||||
Db      61 aatcaaggatgcacatcaaaaggctttgtacacacggaatggccagctcctgctgggaga 120

Qy     156 tcctgttgcagacaactgctgtgcagagaagatctgcacacttcctaacagaggcttgga 215
           |||| | |||||||  |   || |||||||| |||| |  |||||||||  ||||| | ||
Db     121 ccctgattcagacaattatagtccagagaaggtctgtatccttcctaaccgaggcctaga 180

Qy     216 ccgcaccaaggtccccatttcctggggatccagggagggagccgctgcctggcatgtgt 275
           |||| |||||||||||||| ||||||||||| |||||||| ||  |||||||||| |||||
Db     181 ccgctccaaggtccccatcttcctggggatgcagggaggaagttgctgcctggcgtgtgt 240
```

```
Qy    276 ggagacagaagaggggccttccctacagctggaggatgtgaacattgaggaactgtacaa 335
          |||||  ||||||  |||  ||| ||||||||||||||||||| ||||| || |||||
Db    241 aaagacaagagagggacctctcctgcagctggaggatgtgaacatcgaggacctatacaa 300

Qy    336 aggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgccttcag 395
          || |||||| |  |||| || |||||||| |||||||| |||| || || ||||||||
Db    301 gggaggtgaacaaaccacccgtttcacctttttccagagaagcttgggatctgccttcag 360

Qy    396 gcttgaggctgctgcctggcctggctggttcctgtgtggcccggcagagccccagcagcc 455
          |||||||||||||||||| |||||||||| || |||||||| || ||||||||||||||
Db    361 gcttgaggctgctgcctgccctggctggtttctctgtggcccagctgagccccagcagcc 420

Qy    456 agtacagctcaccaaggagagtgagccctcagcccgtaccaagttttactttgaacagag 515
          ||| |||||||||||| |||||||| |||||  ||| |||  | || ||||||||   |||
Db    421 agtgcagctcaccaaagagagtgaaccctccacccatactgaattctactttgagatgag 480

Qy    516 ctggtagggagacaggaaactgcgttttagccttgtgcccccaaaccaagctcatcct 573
          ||||  |||||||  |  |||  |   | | ||  |||||||||  |  || || || |
      481 tcggtaaggagacataaggctggggcctcgtctagtgcccccagtctgagatcttctt 538
```

RESULT 12
AAD11147
ID AAD11147 standard; DNA; 339 BP.
XX
AC AAD11147;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human FIL-1 theta DNA.
XX
KW Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia;
KW insulin dependent diabetes mellitus; lymphoma; microbial infection;
KW ectodermal dysplasia; wrinkly skin syndrome; antisense therapy;
KW tibial muscular dystrophy; inflammation; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..339
FT /*tag= a
FT /product= "Human FIL-1 theta protein"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN WO200155211-A2.

02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02514.
XX
PR 27-JAN-2000; 2000US-0178389.
PR 11-APR-2000; 2000US-0195962.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE;
XX
DR WPI; 2001-457718/49.
DR P-PSDB; AAE05839.
XX
PT isolated FIL-1 theta polypeptide to induce or inhibit the induction of
PT fever and to stimulate the immune system for the treatment of microbial
PT infections -
XX
PS Claim 1; Page 4; 65pp; English.
XX
CC The invention relates to interleukin-1 (IL-1) family ligand designated
CC as FIL-1 theta polypeptides and nucleic acid molecules encoding such
CC polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin
CC dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/
CC lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1
CC theta polypeptides are used to activate and/or inhibit the activation
CC of vascular endothelial cells and lymphocytes; the induction of local
CC tissue destruction and fever; the stimulation of macrophages and
CC vascular endothelial cells to produce IL-6 and the induction of
CC prostaglandins. They are also used to treat inflammation and microbial
CC infections. FIL-1 theta DNA is useful in antisense therapy and gene
CC therapy. The present sequence is a DNA encoding human FIL-1 theta
CC protein.
XX
SQ Sequence 339 BP; 73 A; 96 C; 102 G; 68 T; 0 other;

Query Match 32.9%; Score 335.8; DB 22; Length 339;
Best Local Similarity 99.4%; Pred. No. 1.2e-91;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy    184 aagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctgggg 243
          |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Db      1 aagatctgcatacttcctaacagaggcttggcccgcaccaaggtccccatttttcctgggg 60

Qy    244 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag 120

Qy    304 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc 180

Qy    364 ttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctgg 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctgg 240

Qy    424 ttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccc 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccc 300

Qy    484 tcagcccgtaccaagttttactttgaacagagctggtag 522
          |||||||||||||||||||||||||||||||||||||||
Db    301 tcagcccgtaccaagttttactttgaacagagctggtag 339
```

RESULT 13
AAI70237
ID AAI70237 standard; cDNA; 459 BP.
XX
AC AAI70237;
XX
DT 07-JAN-2002 (first entry)
XX
DE Mouse interleukin-1 receptor antagonist related protein cDNA.
XX
KW Interleukin-1 receptor antagonist related protein; IL-1ra-R; mouse;
KW inhibitor; antiarthritic; antirheumatic; osteopathic;
KW antiinflammatory; neuroprotective; antidiabetic; immunosuppressive;
KW antileprotic; antibacterial; tuberculostatic; anorectic; metabolic;
KW antiviral; hyperglycaemic; nootropic; antiparkinsonian;
KW antidepressant; anticonvulsive; tranquillizer; vulnerary;
KW antiasthmatic; antipsoriatic; dermatological; cytostatic;
KW nephrotropic; antihaemorrhagic; vasotropic; cardiant;
KW antiatherosclerotic; antiinfertility; ophthalmological;
KW gene therapy; diagnosis; ss.
XX
OS Mus musculus.
XX
PN WO200142304-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32940.
XX
PR 10-DEC-1999; 99US-170191P.
PR 09-MAR-2000; 2000US-188053P.
PR 04-APR-2000; 2000US-194521P.
PR 10-APR-2000; 2000US-195910P.

PR 28-NOV-2000; 2000US-0170191.
XX
PA (AMGE-) AMGEN INC.
XX
PI Saris CM, Giles J, Mu SX, Xia M, Bass MB, Craveiro R;
XX
DR WPI; 2001-648140/74.
DR P-PSDB; AAM50220.
XX
PT Novel interleukin-1 receptor antagonist-related polypeptide, its
PT fragment, variant useful for treating rheumatoid arthritis, septicemia,
PT Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
PT uveitis, eczema -
XX
PS Claim 1; Fig 7; 163pp; English.
XX
CC The present sequence is that of the coding region of cDNA encoding a
CC novel murine interleukin-1 receptor antagonist-related polypeptide,
CC IL-1ra-R (see AAM50220), which has interleukin-1 inhibitor activity.
CC The cDNA was obtained from a day 7 mouse embryo cDNA library. The
CC mouse IL-1ra-R gene sequence was also determined (see AAI70238).
CC The invention provides mouse and human IL-1ra-R polypeptides and
CC nucleic acids, as well as selective binding agents, vectors, host
CC cells and methods for producing the IL-1ra-R polypeptides. It also
CC provides pharmaceutical compositions and methods for the diagnosis,
CC treatment, amelioration and/or prevention of diseases, disorders
CC and conditions associated with IL-1ra-R, such as those involving
CC immune system dysfunction, infection, weight disorders, neuronal
CC dysfunction, lung, skin, kidney, bone, vascular system, tumour
CC cells, reproductive system, and eye. The nucleic acids are useful
CC in gene therapy, gene mapping, transgenic animal breeding, and as
CC probes and primers.
XX
SQ Sequence 459 BP; 113 A; 125 C; 119 G; 102 T; 0 other;

Query Match 32.2%; Score 328.4; DB 22; Length 459;
Best Local Similarity 82.3%; Pred. No. 2.5e-89;
Matches 377; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

```
Qy      64 atgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctcta 123
           ||||| ||||| ||||||||||||||||||||||||| ||  ||||| | || |||||| |
Db       1 atgtgctcccttcccatggcaagatactacataatcaaggatgcacatcaaaaggctttg 60

Qy     124 tacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagag 183
           |||||| |  |||||||||| ||| ||||||| |||| | ||||||| |   || |||||
Db      61 tacacacggaatggccagctcctgctgggagaccctgattcagacaattatagtccagag 120

Qy     184 aagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctgggg 243
           ||| |||| |  |||||||||| ||||| | |||||| |||||||||||||| |||||||||
Db     121 aaggtctgtatccttcctaaccgaggcctagaccgctccaaggtccccatcttcctgggg 180

Qy     244 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag 303
           || |||||||| ||  |||||||||| ||||| |||||  |||||| |||  ||| |||
Db     181 atgcagggaggaagttgctgcctggcgtgtgtaaagacaagagagggacctctcctgcag 240

Qy     304 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc 363
           |||||||||||||||| ||||| || ||||| || |||||| |  |||| || ||||||
Db     241 ctggaggatgtgaacatcgaggacctatacaagggaggtgaacaaaccacccgtttcacc 300

Qy     364 ttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctgg 423
           || |||||||| ||||  || || ||||||||||||||||||||||||||| |||||||||
Db     301 tttttccagagaagcttgggatctgccttcaggcttgaggctgctgcctgccctggctgg 360

Qy     424 ttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccc 483
           || || |||||||| || ||||||||||||||||| |||||||||| |||||||| |||
Db     361 tttctctgtggcccagctgagccccagcagccagtgcagctcaccaaagagagtgaaccc 420

Qy     484 tcagcccgtaccaagttttactttgaacagagctggta 521
           ||  ||| |||  | || ||||||||   |||  ||||
Db     421 tccacccatactgaattctactttgagatgagtcggta 458
```

RESULT 14
AAA89180
ID AAA89180 standard; cDNA; 459 BP.
XX
AC AAA89180;
XX
DT 19-MAR-2001 (first entry)
XX
DE Mouse interleukin-1 Hy2 cDNA.
XX
KW Interleukin-2 Hy2; IL-1 Hy2; mouse; interleukin-1 receptor;
KW antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW antitumour; antiinflammatory; diagnosis; therapy; ss.
XX
OS Mus sp.
XX
PN WO200071719-A1.
XX
PD 30-NOV-2000.
XX
PF 22-MAY-2000; 2000WO-US14144.
XX
PR 20-MAY-1999; 99US-0316086.
PR 10-MAR-2000; 2000US-0522964.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ballinger DG, Ford J, Ho AS, Lin HS, Pace AM;
XX
DR WPI; 2001-016409/02.
DR P-PSDB; AAB19925.
XX
PT New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT preventing and treating disorders, such as cancers and inflammatory
PT diseases -
XX
PS Example 9; Page 152; 158pp; English.
XX
CC The present sequence is that of mouse cDNA encoding interleukin-1 Hy2
CC (IL-1 Hy2, see AAB19925), a novel member of the interleukin-1 receptor
CC antagonist family. The sequence is predicted from isolated IL-1 Hy2
CC genomic DNA (see AAA89177). The predicted mouse and human (see
CC AAB19922) IL-1 Hy2 polypeptides share 81.7% homology. The murine
CC genomic DNA can be used to generate transgenic animals which overexpress
CC IL-1 Hy2 protein or have the IL-2 Hy2 gene knocked out. Human
CC IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers
CC involving elevated levels of IL-1, such as breast adenocarcinoma,
CC brain tumours, melanoma, giant cell tumours of bone, acute
CC myelogenous leukaemia, oral epidermoid carcinoma or squamous cell
CC carcinoma, and inflammatory disease mediated by interleukin-18 (all
CC claimed).
XX
SQ Sequence 459 BP; 113 A; 125 C; 119 G; 102 T; 0 other;

Query Match 32.2%; Score 328.4; DB 22; Length 459;
Best Local Similarity 82.3%; Pred. No. 2.5e-89;
Matches 377; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

```
Qy      64 atgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctcta 123
           ||||| ||||| ||||||||||||||||||||||||| ||  ||||| | || |||||| |
Db       1 atgtgctcccttcccatggcaagatactacataatcaaggatgcacatcaaaaggctttg 60

Qy     124 tacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagag 183
           |||||| |  |||||||||| ||| ||||||| |||| | ||||||| |   || |||||
Db      61 tacacacggaatggccagctcctgctgggagaccctgattcagacaattatagtccagag 120

Qy     184 aagatctgcacacttcctaacagaggcttggaccgcaccaaggtccccatttttcctgggg 243
           ||| |||| |  |||||||||| ||||| | |||||| |||||||||||||| |||||||||
Db     121 aaggtctgtatccttcctaaccgaggcctagaccgctccaaggtccccatcttcctgggg 180
```

```
Qy    244 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag 303
          || |||||||| ||  |||||||||| |||||  |||||  |||||| |||  ||| |||
Db    181 atgcagggaggaagttgctgcctggcgtgtgtaaagacaagagagggacctctcctgcag 240

Qy    304 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc 363
          |||||||||||||||||| ||||| || ||||| || |||||| |  |||| || ||||||
Db    241 ctggaggatgtgaacatcgaggacctatacaagggaggtgaacaaaccacccgtttcacc 300

Qy    364 ttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctggcctggctgg 423
          || |||||||| |||| || || ||||||||||||||||||||||||| |||||||||
Db    301 tttttccagagaagcttgggatctgccttcaggcttgaggctgctgcctgccctggctgg 360

Qy    424 ttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgagccc 483
          || || |||||||| || ||||||||||||||||| ||||||||||| |||||||| |||
Db    361 tttctctgtggcccagctgagccccagcagccagtgcagctcaccaaagagagtgaaccc 420

Qy    484 tcagcccgtaccaagttttactttgaacagagctggta 521
          ||  ||| |||  | || |||||||||   |||  ||||
      421 tccacccatactgaattctactttgagatgagtcggta 458
```

```
RESULT  15
AAA89179
ID   AAA89179 standard; DNA; 4388 BP.
XX
AC   AAA89179;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Mouse interleukin-1 Hy2 gene.
XX
KW   Interleukin-2 Hy2; IL-1 Hy2; mouse; interleukin-1 receptor;
KW   antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma;
KW   myeloma; giant cell tumour of bone; acute myelogenous leukaemia;
KW   oral epidermoid carcinoma; squamous cell carcinoma; inflammation;
KW   antitumour; antiinflammatory; diagnosis; therapy; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1393..3939
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   intron          1425..2915
FT                   /*tag=  b
FT   exon            2916..3001
FT                   /*tag=  c
     intron          3002..3333
                     /*tag=  d
FT   exon            3334..3461
FT                   /*tag=  e
FT   intron          3462..3726
FT                   /*tag=  g
FT   exon            3727..3939
FT                   /*tag=  h
XX
PN   WO200071719-A1.
XX
PD   30-NOV-2000.
XX
PF   22-MAY-2000; 2000WO-US14144.
XX
PR   20-MAY-1999;   99US-0316086.
PR   10-MAR-2000; 2000US-0522964.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Ford J,  Ho AS,  Lin HS,  Pace AM;
XX
DR   WPI; 2001-016409/02.
DR   P-PSDB; AAB19925.
XX
PT   New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing,
PT   preventing and treating disorders, such as cancers and inflammatory
PT   diseases -
XX
PS   Example 9; Page 149-151; 158pp; English.
XX
CC   The present sequence is that of mouse genomic DNA encoding
CC   interleukin-1 Hy2 (IL-1 Hy2, see AAB19925), a novel member of the
CC   interleukin-1 receptor antagonist family.  The DNA was obtained by
CC   screening a commercial mouse BAC library with IL-1 Hy2 cDNA.  Exons
CC   were predicted using GenScan software.  The mouse and human (see
CC   AAB19922) IL-1 Hy2 polypeptides share 81.7% homology.  The genomic
CC   DNA can be used to generate transgenic animals which overexpress
CC   IL-1 Hy2 protein or have the IL-2 Hy2 gene knocked out.  Human
CC   IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers
CC   involving elevated levels of IL-1, such as breast adenocarcinoma,
CC   brain tumours, melanoma, giant cell tumours of bone, acute
CC   myelogenous leukaemia, oral epidermoid carcinoma or squamous cell
CC   carcinoma, and inflammatory disease mediated by interleukin-18 (all
CC   claimed).
XX
SQ   Sequence 4388 BP; 1179 A; 1051 C; 935 G; 1223 T; 0 other;
```

```
  Query Match             20.0%;  Score 204.4;  DB 22;  Length 4388;
  Best Local Similarity   74.3%;  Pred. No. 3.9e-51;
  Matches  284;  Conservative    0;  Mismatches   96;  Indels    2;  Gaps    2;

Qy     295 tccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccaca 354
           |||||    |   |||||||||||||| ||||| || ||||| || |||||| |  ||||
Db    3712 tccctttccccacaggatgtgaacatcgaggacctatacaagggaggtgaacaaaccacc 3771

Qy     355 cgcttcaccttcttccagagcagctcaggctccgccttcaggcttgaggctgctgcctgg 414
           || |||||||| |||||||| ||||  || || ||||||||||||||||||||||||||
Db    3772 cgtttcacctttttccagagaagcttgggatctgccttcaggcttgaggctgctgcctgc 3831

Qy     415 cctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaaggag 474
           |||||||||||  || |||||||| || ||||||||||||||||| ||||||||||| |||
Db    3832 cctggctggtttctctgtggcccagctgagccccagcagccagtgcagctcaccaaagag 3891

Qy     475 agtgagccctcagcccgtaccaagttttactttgaacagagctggtagggagacaggaaa 534
           |||||  |||||  |||  |||  |  || ||||||||   |||  ||||  ||||||  |
Db    3892 agtgaaccctccacccatactgaattctactttgagatgagtcggtaaagagacataagg 3951

Qy     535 ctgcgttttagccttgtgccccccaaaccaagctcatcctgctcagggtctatggtaggca 594
           ||| |   | | || |||||||||  |  || || || |||||||  ||| ||| | |||
Db    3952 ctggggcctcgtctagtgcccccagtctgagatcttcttgctcagcatctctggaaagca 4011

Qy     595 gaataatg-tcccccgaaatatgtccacatcctaatcccaag-atctgtgcatatgttac 652
           |||||| |      | ||| ||||     || |||||||| || |||||||    ||||||
Db    4012 gaataaggaagataccaaagatgtttgggtcttaatccccagaatctgtgaccgtgttac 4071

Qy     653 catacatgtccaaagaggtttt 674
             || ||| | || |   ||||
Db    4072 attaaatggcaaagggattttt 4093
```

```
Search completed: May 19, 2002, 09:27:01
Job time: 5526 sec
```